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Result
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Maximum Match 10
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Maximum DB
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length: 2000000000
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                Ig heavy chain V-I
Ig heavy chain V r
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Ig heavy chain V r
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90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3	90.3
314	312	309	261	258	254	253	246	226	220	216	204	191	190	190	180
N	N	N	N	N	N	N	N	N	N	N	N	N	2	N	N
AC2690	I48303	S43573	A34476	B61228	E83619	I48304	I48302	T29404	B49736	A72291	B82166	S43178	A54518	A45601	T39395
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S26460
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Uan-1995 #sequence_revision 06
C;Accession: $26460
R;Kavaler, J.
submitted to the EMBL Data Library, Aprinaperion of the EMBL
A;Reference number: S264
A;Accession: S26460
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-101 <KAV>
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J. Exp. Med. 168, 229-245, 1988
A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobuling hyperenters. PLO116; MUID:88286083; PMID:2840480
A;Reference number: PLO116; MUID:88286083; PMID:2840480
A;Residues: 1-98 <BIR>
A;Rote: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement in the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement in the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement in the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement in the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement in the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement in the sequence of the sequence
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A;Molecule type: DNA
A;Residues: 1-98 <TOM>
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C; Superfamily:
C; Keywords: het
F;7-90/Domain:
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J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1655
                                                          RESULT 5
S38714
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                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-114 <GRI>
A;Cross-references: EMBL: Z18822
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revisio
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A;Accession: S36280
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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, EMBO J. 12, 725-734, 1993

A;Title: Human anti-self antibodies with high specificity from phage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
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C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1655
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#sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
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0; Mismatches
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-115 <CIM>
A;Residues: 1-115 <CIM>
A;Cross-references: EMBL:X76014; NID:g416092; PIDN:CAA53601.1; PID:g1334076
A;Cross-references: EMBL:X76014; V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;14-99/Domain: immunoglobulin homology <IMM>
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                                                                                                                      C;Accession: S60299; S17079

R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A. Immunol. Lett. 34, 57-62, 1992

A;Title: Immunoglobulin heavy and light chain gene sequences A;Reference number: S60295; MUID:93122853; PMID:1282498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C;Accession: S78486; S31115
R;Raaphorst, F.M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S78486
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S78486
                                                                                                                                                                                                                                Ig heavy chain V-gene (clone HHG19) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IVM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X62965
A;Experimental source: clone FL13-28
R;Raaphorst, F.M.; Timmers, E.; Kente
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R;Cimanis, A.Y.
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A;Residues: 1-4,'L',6-32,'G',34-52,'E',54-73,'K',75-97 <RAW>
A;Cross-references: EMBL:X62965
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                                        A;Residues:
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                                                               A; Molecule type: DNA
                      A;Cross-references:
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-references: EMBL:X62128; NID:g38340; PIDN:CAA44059.1; the authors did not translate the codons for residues
                                                                                                                                                                                                                                                                                                                                                                                                  31 SYWMS 35
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R;Hsu, E.; Schwager, J.; Alt, F.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 8010-8014, 1989
A;Title: Evolution of immunoglobulin genes: V-H families
A;Reference number: A33989; MUID:90046727; PMID:2510156
A;Accession: A33989
                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V-1-D-J region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
A;Introns: 16/1
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                   F;15-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                  A;Residues: 1-122 <HSU>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Nuclelc Acids Res. 15, 5888, 1987
A;Title: Nucleotide sequences of variable region segments of
A;Reference number: S00700; MUID:87289054; PMID:3112743
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A;Note: the sequence was determined from the germline gene
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A; Residues: 1-118 < YAM>
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C;Species: Xenopus laevis (African clawed fro
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Pred. No. 49;
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RESULT 10

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A;Cross-references: EMBL:X67908; NID:g33580; PIDN:CAA48106.1; PC;Superfamily: immunoglobulin V region; immunoglobulin homology F;35-118/Domain: immunoglobulin homology <IMM>
                                                                     A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <RES>
                                                                                                                                        R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37781
                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change
C;Accession: 13781: M.
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A;Cross-references: EMBL:Z14189; NID:g31005; PIDN:CAA78558.1; PID:g31006 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A; Accession: S31587
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A;Description: Mechanisms that generate human immunoglobulin diversit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z14175; NID:g31015; PIDN:CAA78544.1; FC;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999 C;Accession: S31675
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A; Accession: S31675
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A;Experimental source: strain 1021, megaplasmid pSymB
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.; L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K. A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: 137780
A;Accession: 137780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable aldehyde or xanthine dehydrogenase, iron-sulfur subunit protein [imported] C;Species: Sinorhizobium meliloti C;Species: Sinorhizobium meliloti C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001 C;Accession: F95966 C;Accession: F95966 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; He Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
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A; Residues: 1-147 < RES>
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C;Species: Homo saplens (man)
C;Date: 16-Feb-1996 #text_change
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A;Title: The complete sequence of the 1,693-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: F95966
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A;Molecule type: DNA
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Pred. No. 55;
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Pred. No. 81;
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Mismatches
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RESULT 15
AE2275
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A;Molecule type: DNA
A;Molecule type: CNA
A;Residues: 1-939 - KNIR>
A;Cross-references: GB:BA000019; PIDN:BAB75455.1; PID:g17132890; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                      DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Kaneko, T.; Nakamura, Y.; Wolk, Nakazaki, N.; Shimpo, S.; Sugimo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein alr3756 [imported] - Nostoc ep. (strain PCC 7120)
C;Species: Nostoc ep. PCC 7120
A;Note: Nostoc ep. strain PCC 7120 is a synonym of Anabaena ep. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
Search completed: January 12, 2004, 07:02:57 Job time: 7.53125 secs
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S.; Sugimoto, M.; Takaza
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Pred. No. 3
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Takazawa, M.; Yamada,
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, M.; Yasuda, M.; Tabata,
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                                                        "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein specifically catalyzes the removal of
signal peptides from prolipoproteins (By similarity).
-!- CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from
membrane prolipoproteins. Hydrolyses Xaa-Xbb-Xcc-|-Cys, in which
Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc
is often Gly or Ala, and the Cys is alkylated on sulfur with a
diacylglyceryl group.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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Transferase; DNA-directed DNA polymerase; DNA replication; DNA-binding; Mitochondrion; Magnesium.
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Bacteria; Proteobacteria;
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copyright. It is produced through a collaboration tute of Bioinformatics and the EMBL outstation -
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MEDLINB-22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Kubota Y.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahaemolyticus: a pathogenic
distinct from that of V. cholerae.";
Lancet 361:743-749(2003).
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Lipoprotein signal peptidase (EC 3.4.23.36)
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InterPro; IPR001872; SigPTase_A8.
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Bacteria; Proteobacteria;
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                                                                                                   FUNCTION: This protein specifically catalyzes the removal of signal peptides from prolipoproteins (By similarity).

CATALYTIC ACTIVITY: Cleavage of N-terminal leader sequences from membrane prolipoproteins. Hydrolyses Xaa-Xbb-Xcc-|-Cys, in which Xaa is hydrophobic (preferably Leu), Xbb is often Ser or Ala, Xcc is often Gly or Ala, and the Cys is alkylated on sulfur with a diacylglyceryl group.

SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bloinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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PROSITE; PS00855; SPASE_II; 1.
Hydrolase; Aspartyl protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AP005074; BAC58798.1; -.
                                                                                                                                                                                                                                                                                                              STRAIN=972;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4896
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                                                                                                                                                                                                                                                                                                  MEDLINE=21848401; PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces.
OLIGORIBONUCLEOTIDES (F
         FUNCTION: 3'-TO-5' EXORIBONUCLEASE SPECIFIC FOR SMALL OLIGORIBONUCLEOTIDES (BY SIMILARITY).
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80.0%;
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BY SIMILARITY.
BY SIMILARITY.
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OLIGORIBONUCLEASE FAMILY.
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EMBL; M29837; EMBL; M37003;

AAA29856.1; AAA29922.1;

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P14202;
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TEGU_S
                                         modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                     This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                             protectively vaccinated with isolated tegumental surface membranes. Mol. Biochem. Parasitol. 46:159-168 (1991).

-i- TISSUE SPECIFICITY: ADULT TEGUMENT.

-i- DEVELOPMENTAL STAGE: THIS ANTIGEN OCCURS IN ADULTS & SPOROCYSTS

-BUT NOT IN CERCARIAE, EGGS OR NEWLY TRANSFORMED SCHISTOSOMULA.

IT IS A DEVELOPMENTALLY REGGULATED PROTEIN.

-i- SIMILARITY: TO S.MANSONI ANTIGEN SM21.7.
                                                                                                                                                                                                                                                                                                                                                                                           Stein L.D., David J.R.; "Cloning of a developmentally regulated tegument antigen Schistosoma mansoni.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAM-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Tegument antigen (I(H)A) (Antigen SMA22.6) (A
Schistosoma mansoni (Blood fluke)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                      "Molecular cloning and characterisation of the 22-kilodalton adult Schistosoma mansoni antigen recognised by antibodies from mice
                                                                                                                                                                                                                                                                                                     Jeffs S.A., Hagan
Simpson A.J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; Hydrolase; Exonuclease; Nuclease ACT_SITE 130 130
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                                                        (See http://www.isb-sib.
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RESULT 6
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28-FEB-2003
28-FEB-2003
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01-FEB-1995
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or send a
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SEQUENCE
                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
Periplasmic protein torT precursor.
TORT OR Z1411 OR ECS1149.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce
Enterobacteriaceae;
NCBI_TaxID=83334;
{1}
                                                                                                                                                                                                                                                                                          WormPep; C05B5.4; CEC
Hypothetical protein.
SEQUENCE 315 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A54518; A54518.
InterPro; IPR002048; E
Pfam; PF00036; efhand;
SMART; SM00054; EFh; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mortimore B.J.;
Submitted (APR-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00018; EF_HAND; UNKNOWN_1.
                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                              PIR;
                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
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135.9
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31, Last sequ
32, Last anno
kDa protein C
                       Escherichia.
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80.0%;
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protein C05B5.4 in chromosome
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                                 Gammaproteobacteria;
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                                                                                                                                                                                                                                          Score 28; DB 1;
Pred. No. 1.9e+02;
1; Mismatches 0
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Pred. No. 1.2e+02;
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                                    Enterobacteriales;
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RESULT 8
TORT ECOLI STANDARD; PRT; 342 AA
ID TORT ECOLI STANDARD; PRT; 342 AA
AC P3868; P75888;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation updat
DE Periplasmic protein torT precursor.
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C MEDLINE-21156231; PubMed=11258796;
A Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama A. Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T., A. Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T. "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli "Complete genomic comparison with a laboratory strain K-12.";
DIA Res. 8:11-22 (2001).
L DNA Res. 8:11-22 (2001).
L DNA kes. 8:11-22 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001761; PeriplaBP/Lac1.
Pfam; PF00532; Peripla BP like; 1.
Transport; Periplasmic; Signal; Complete proteome SIGNAL
1 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                        Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE005293; AAG55541.1; -. EMBL; AP002554; BAB34572.1; -.
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Nature 409:529-533(2001).
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STRAIN=0157:H7
                                                                            Enterobacteriaceae;
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SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECEPTOR FAMILY 2.
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E90772; E90772
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37950 MW;
                                                                               Escherichia
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                                                                                                     Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 28; DB 1; L
Pred. No. 2.1e+02;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PERIPLASMIC PROTEIN 8844A18064D8A54D (
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                                                                                                                                                                                                                 update)
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SEQUENCE FROM N.A

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto I Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The periplasmic TorT protein is required for t reductase gene induction in Escherichia coli.";

Bacteriol. 178:1219-1223(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAINEK12 / MC4100;
MEDLINE=94364937; Pubmed=8083154;
Simon G., Mejean V., Jourlin C., Chippaux M., Pascal M.-C.;
"The tork gene of Escherichia coli encodes a response regulator
protein involved in the expression of the trimethylamine N-oxide
                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corresponding to the 12.7-28.0 min
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                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia
                                                                                                                                                          SIGNAL
                                                                                                                                                                            fransport;
                                                                                                                                                                                                                                       EcoGene; EG12616; torT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97061202; PubMed=8905232;
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                                                                                                                                                                                                                nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Upon binding a putative inducer it probab with torS and allows it to play a role in the inductorCAD operon for trimethylamine N-oxide reductase. SUBCCELLULAR LOCATION: Periplasmic.
SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECEPTOR FAMILY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence of Escherichia coli K-12.", nce 277:1453-1474 (1997).
                                                                                                                                                                                                                                                           H64840; H64840
                                                                                                                                                                                                                                                                                                                                    X94231; CAA63921.1; --.
                                                                                                                                                                                                                                                                       AE000201; AAC74079.1; -. D90736; BAA36136.1; -. D90737; BAA35761.1; -.
                                                                                                                                                                                                PF00532;
                                                                                                               Similarity 4; Conserv
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342
  Conservative
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37864 MW;
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                    90.3%;
                                                                                             PERIPLASMIC I
W -> S (IN RI
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Score
Pred.
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  Mismatches
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on the lin
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                                      Length 342;
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  Indels
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DNLI BP1
P00969;
                   EMBL; V01124; CAA24322.1;
EMBL; V01126; CAA24326.1;
EMBL; V01127; CAA24336.1;
                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLLNE=9622302; PubMed=8653795;
Subramanya H.S., Doherty A.J., Ashford
"Crystal structure of an ATP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn J.J., Studier F.W.;
"Nucleotide sequence from the genetic
DNA to the beginning of gene 4.";
J. Mol. Biol. 148:303-330(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dunn J.J., Studier F.W.;
"Complete nucleotide sequence of bacteriophage T7
locations of T7 genetic elements.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, T7-like viruses.
                                                                                                                                                                                                              between the Swiss Institute of Bioinfo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-81054683; PubMed=6254001;
Saito H., Tabor S., Tamanoi F., Richardson C.C.;
"Nuclectide sequence of the primary origin of bacteriophage replication: relationship to adjacent genes and regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn J.J., Studier F.W.; "The transcription termination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUL-1986
28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elements.";
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MEDLINE=81053683; PubMed=7001354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10760;
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                                                                                                                                                                                                                                                                                                                                  FUNCTION: DNA LIGASE, WHICH IS EXPRESSED IN THE EARLY STAGE OF LYTIC DEVELOPMENT, HAS BEEN IMPLICATED IN T7 DNA SYNTHESIS AND GENETIC RECOMBINATION. IT MAY ALSO PLAY A ROLE IN T7 DNA REPAIL CATALYTIC ACTIVITY: ATP + {deoxyribonucleotide}(N) + {deoxyribonucleotide}(M) = AMP + diphosphate + {deoxyribonucleotide}(N+M).
                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE ATP-DEPENDENT DNA LIGASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ligase
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                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85:607-615(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad.
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(Rel. 01, Last sequence update)
(Rel. 41, Last annotation update)
(EC 6.5.1.1) (Polydeoxyribonucleotide)
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PDB; 1A01; 25-MAR-98.

InterPro; IPR00977; DNA_ligase.

Pfam; PP01068; DNA_ligase; 1.

PROSITE; PS00697; DNA_LIGASE_A1; 1

PROSITE; PS00333; DNA_LIGASE_A2; 1

PROSITE; PS00333; DNA_LIGASE_A3; 1

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EMBL; Z99123; CAB15853.1; -
PIR; S39683; S39683;
Subtilist; BG10574; ywbM.
Pfam; PF04302; DUF451; 1.
Hypothetical protein; Compl
SEQUENCE 385 AA; 42796 M
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NCBI_TaxID=1423;
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RX KEDLINE=98044033; PubMed=9384377;
RX KEDELINE=98044033; PubMed=9384377;
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borniss R., Boursier L., Brans A., Edward M., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Chim S.Y., Glaser P., Coffeau A., Edrich S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Ghim S.Y., Glaser P., Koningstein G., Krogh S., Kumano M.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P., Tognoni A.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT Teheritis "."
The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95020537; PubMed=7934828; Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W., Hullo M.F., Ionsecu M., Lubochineky B., Marcelino L., Moszer I. Presecan E., Santana M., Schneider E., Schweizer J., Vertes A., Rapoport G., Danchin A.; "Bacillus subtilis genome project: cloning and sequencing of the bregion from 325 degrees to 333 degrees."; Mol. Microbiol. 10:371-384(1993).
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Hypothetical protein
YWBM OR IPA-28D.
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RESULT 11 Y306_MYCGI

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(Rel. 33, Created)

MG306.

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protein MG306.

Mycoplasma

genitalium.

Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma

SEQUENCE FROM N.A.
STRAIN=ATCC 33530 / G-37;
MEDLINE=96026346; PubMed=7569993;

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                        Hypothetical SPAC11D3.06.
Schizosaccharomyces pombe (Fission yeast)
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                                           protein C11D3.06 in chromosome
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Roben J., Grymonprez B.,
Waltiens I., Vanstreels E., Rieger M., Schaefer M., Weller-Auer S.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Weller H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Rager P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
The genome sequence of Schizosaccharomyces pombe.";
RL Janger J., Subcellullar Location: Integral membrane protein (Potential).
CC - SIMILARIY: BEIONGS TO THE MULTI ANTIMICROBIAL EXTRUSION (MATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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Query Match Best Local S Matches 4 TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM TRANSMEM Hypothetical protein; TRANSMEM 4 2 InterPro; IPR002528; MatE. Pfam; PF01554; MatE; 2. TIGRFAMs; TIGR00797; matE; 1. GeneDB_SPombe; SPAC11D3.06; TRANSMEM TRANSMEM TRANSMEM T37517; T37517 4; Similarity Conservative A A 49086 90.3%; Transmembrane; Tr 4 POTENTIAL. MW; Score 28; DB Pred. No. 2.8e 1; Mismatches POTENTIAL.
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196 SYWLS 1 SYWMS

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RESULT 13
CA34_BOVIN
   membrane collagen.";
J. Biol. Chem. 262:7874-7877(1987).
-i- FUNCTION: TYPE IV COLLAGEN IS T.
GLOMERULAR BASEMENT MEMBRANES (MESHWORK TOGETHER WITH LAMININS
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=88330844; PubMed=3417661; Saus J., Wieslander J., Langeveld J.P.M., Quinones S., Hudson B.G.; "Identification of the Goodpasture antigen as the alpha 3(IV) chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91093146; PubMed=1985905; Morrison K.E., Germino G.G., Reeders S.T.; "Use of the polymerase chain reaction to clone and sequence a cDNA encoding the bovine alpha 3 chain of type IV collagen.";
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01-NOV-1997
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01-NOV-1997
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Butkowski R.J., Langeveld J.P.M., Wieslander J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 227-244.
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MEDLINE=88330844; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gunwar S., Saus J., Noelken M.E., Hudson B.G.;
"Glomerular basement membrane. Identification of a fourth chain, alpha 4, of type IV collagen.";
1. Biol. Chem. 265:5466-5469(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 227-258.
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Bovidae; Bovinae; Bo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Localization of the Goodpasture epitope to
                                                                                                                                 WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN MITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN MITAL).

SUBCELLULAR LOCATION: CELL SURFACE (POTENTIAL).

DOMAIN: ALPHA CHAINS OF TYPE IV COLLAGEN HAVE A NONCOLLAGENOUS DOMAIN (NCI) AT THEIR C.-TERMINUS, FREQUENT INTERRUPTIONS OF THE GAY Y REPEATS IN THE LONG CENTRAL TRIPLE-HELICAL DOWAIN (WHICH MAY CAUSE FLEXIBILITY IN THE TRIPLE HELIX), AND A SHORT N-TERMINAL TRIPLE-HELICAL 75 DOMAIN.

- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.

- PTM: Type IV collagens contain numerous cysteine residues which are involved in inter- and intramolecular disulfide bonding. 12 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              collagen IV.";
Biol. Chem. 263:13374-13380(1988).
                                                                                                         SIMILARITY: TO OTHER TYPE IV COLLAGENS
                                                                                                                                                                                                                                                                                                                                   NIDOGEN.
SUBUNIT: THERE ARE SIX TYPE IV COLLAGEN ISOFORMS, ALPHA 1
ALPHA 6(IV), EACH OF WHICH CAN FORM A TRIPLE HELIX STRUCT
WITH 2 OTHER CHAINS TO GENERATE TYPE IV COLLAGEN NETWORK.
                                                                                                                            these, IV col
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(Rel. 35,
(Rel. 35,
pha 3(IV)
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35, Last sequence update)
35, Last annotation updat
(IV) chain (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    annotation update) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                               LAMININS,
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30-MAY-2000
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                                                                                                                            Mandon K., Michel-Reydellet N., Encarnacion S., Kamu
Leija A., Cevallos M.A., Elmerich C., Mora J.;
"Poly-beta-hydroxybutyrate turnover in Azorhizobium
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Pfam; PF01391; Collagen;
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        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                       STRAIN=ORS571;
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                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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                                                                                                                                                                                                             Hyphomicrobiaceae;
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Pred. No. 2.9e+02;
1; Mismatches (
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NONHELICAL REGION (NC1)
CELL ATTACHMENT SITE (P
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C03B66F14E7008DE
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Q63517;
01-NOV-1997
01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STIMULATING HORMONE.

STIMULATING HORMONE.

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, OVARY AND SPLEEN.

-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS, OVARY AND SPLEEN.

A WUCH LOWER MENA LEVEL IS FOUND IN BRAIN AND LUNG, AND NO EXPRESSION IS DETECTED IN LIVER, KIDNEY, HEART, MUSCLE, PITUITARY EXPRESSION IS DETECTED IN LIVER, KIDNEY, HEART, MUSCLE, PITUITARY GLAND, PROSTATE, EPIDIDYMIS AND SEMINAL VESICLE.

-!- INDUCTION: BY FOLLICLE-STIMULATING HORMONE (FSH).
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PHB biosynthesis; Transferase; Acyltransferase.
ACT_SITE 320 320 POTENTIAL.
                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                 EMBL; X90355; CAA62018.1; -. PIR; I57665; I57665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRPR1, a primary response gene encoding a leucine-rich protein.";
Mol. Cell. Endocrinol. 108:115-124(1995).
-!- FUNCTION: INVOLVED IN THE RESPONSE OF GONADAL TISSUES TO FOLLICLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE=Testis;
MEDLINE=95278605; PubMed=7758824;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
28.FEB-2003 (Rel. 41, Last annotation update)
Leucine-rich primary response protein 1 (Follicle-stimulating hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Regulation of gene expression in Sertoli cells by follicle-stimulating hormone (FSH): cloning and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Slegtenhorst-Eegdeman K.E., Post M., Baarends W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       primary response protein).
FSHPRH1 OR LRPR1.
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[1]
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383 SYWLS 387
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Pred. No. 4.6e+02;
1; Mismatches 0
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Pred. No.
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Sciurognathi; Muridae; Murinae; Rattus.
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Search completed: January 12, 2004, 06:59:35 Job time : 5.73438 secs

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Result
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                                                                                                                                                                                                                                              Score
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_fungi:*
4: sp_invertebrate
6: sp_mammal:*
6: sp_macmal:*
9: sp_bage:*
10: sp_bage:*
11: sp_votent:*
12: sp_virus:*
12: sp_virus:*
13: sp_vertebrate
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Q9ulb6 homo sapien
Q9zut9 rhizobium m
Q8nrh2 corynebacte
Q8fq16 corynebacte
Q8yqr3 anabaena sp
Q9518 arabidopsis
Q955k1 mytilus tro
Q8lxs7 mytilus edu
Q8lxs9 mytilus edu
Q8lxs9 mytilus edu
Q8lxs0 mytilus edu
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72 cani	Q26511 schistosoma					v	ostrinia	str	div	Q61430 mus musculu	yti:	ytilus	ytilus	Q955k3 mytilus edu	ytilus	mytilus	Q94nc1 mytilus tro		Q9ffy3 arabidopsis			mytilus		pyrococ	a5 myti:	homo sa	myti.	Q8lxr8 mytilus gal

ALIGNMENTS

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y 1 SYWMS 5 	Query Match 100.0%; Score 31; DB 4; Length 95; Best Local Similarity 100.0%; Pred. No. 99; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 95 AA; 1	NON TER 95 9		PROSITE:	Pfam; PF00047; 19; 1	InterPro; IPR003596;	<pre>InterPro; IPR003006;</pre>	InterPro; IPR007110;							N [1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates;			VH.	<pre>Imunoglobulin heavy chain (Fragm</pre>	01-MAR-2003 (TrEMBLrel. 23, Last annotation	01-MAY-2000 (TrEMBLrel.	01-MAY-2000 (TrEMBLrel. 13, Created)		D Q9ULB6 PRELIMINARY; PRT; 95 AA.	OSITIBE	

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RESULT
Q8NRH2
                   DR REIT OR RECEPTION OF THE PROPERTY OF THE PR
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A Golding B., Puehler A.;

AT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti.";

AT Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).

BR InterPro; IPR002888; ZPe-ZS bind.

InterPro; IPR002888; ZPe-ZS bind.

InterPro; IPR006051; ZPe-ZS bind.

InterPro; IPR006011; Farredoxin.

DR InterPro; IPR00611; Tat.

DR Pfam; PF00111; Fer2; 1.

DR Pfam; PF01799; fer2 2; 1.

DR Pfam; PF01799; fer2 2; 1.

DR ProDom; D1166071; ZFe-ZS bind; 1.

PR PTIGRRAMS; TIGR01409; TAT signal seq; 1.

DR PROSITE; PS00197; ZPEZS FERREDOXIN; 1.

KW Plasmid; Hypothetical protein; Complete proteome.

KW Plasmid; Hypothetical protein; Complete proteome.
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Best Local
       "Complete genomic sequence of Corynebact Submitted (MAY-2002) to the EMBL/GenBank EMBL, AP005277; BAB98470.1; -
InterPro; IPR000733; Flav monooxygnse. InterPro; IPR002938; Moxy FAD binding. InterPro; IPR003042; Rng_mnoxygenase. Pfam; PF01494; FAD binding_3; 1.
Pfam; PF01360; Monooxygenase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QBNRHI;
QBNRHI;
QBNRHI;
QBNRHI;
Q1-QCT-2002 (TrEMBLrel. 22, Created)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent
Q-vidoreductases (EC 1.14.13.2).
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01-DEC-2001
01-DEC-2001
01-MAR-2003
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Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium glutamicum (Brevibacterium flavum).
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN=ATCC 13032
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(TrEMBLrel. 19, Last sequence update)
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dehyde or xanthine dehydrogenase, iron-sulfur subunit
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EMBL/GenBank/DDBJ
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Pred. No. 2.1e+02;
; Mismatches 0;
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Q8YQR3;
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01-MAR-2002
01-MAR-2002
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Q8FQ16;
01-MAR-2003
                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDIINE=21595285; PubMed=11759840;
MEDIINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasar Kaneko T., Nakamura Y., Wolkim, Ishikawa A., Kawashima K
Watanabe A., Iriguchi M., Ishikawa A., Matsumoto M., Matsuno A., M
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Nida Y., Kohara M., Matsumoto M., Takazawa M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2002) to the ENBL; AP005217; BAC17943.1; -
                                                                                                                                                                Watanabe A., Iriguchi M., Ishikav Kishida Y., Kohara M., Matsumoto Nakazaki N., Shimpo S., Sugimoto Yasuda M., Tabata S.; "Complete genomic sequence of the "Complete genomic sequence of the cyanobacterium Anabaena sp. strai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monooxygenase;
SEQUENCE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
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                           Hypothetical protein;
SEQUENCE 939 AA; 10
                                                                                              DNA Res. 8:205-213(2001).
EMBL; AP003594; BAB75455.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
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5; Conserv
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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AA; 44008 MW; C6E
in; Complete 104233 MW:
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44698 MW; 6E
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100.0%; F
tive 0;
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Pred. No.
                   proteome.
8FE0A7CA6C1759A5
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nitrogen-fixing

CRC64;

Sasamoto Muraki A.,

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Nostoc.

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Corynebacterium efficiens.
Bacteria; Actinobacteridae; Actinomycet
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_TaxID=152794;
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Oxidoreductase; Complete prote
SEQUENCE 395 AA; 44008 MW;
                                                                                                                                                       STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
Kawarabayasi Y., Yamazaki J., Hino Y., Kikuchi H.,
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi
Usuda Y., Sugimoto S.;
                                                                                                                      "The entire genomic sequence of Corynebacterium efficiens submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                            Actinobacteridae; Actinomycetales;
                                                                                                                                                                                                                                                                                                                                                               3-monooxygenase.
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Last annotation update)
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Mismatches
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4e+02;
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A., Nishio
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Pfam; PF01369; Sec7; 1.
SMART; SM00233; PH; 1.
SMART; SM00222; Sec7; 1.
                                                                                                                           Barrell B.G., Rajandream M.A.,
Submitted (AUG-1997) to the EN
-!- SIMILARITY: CONTAINS 1 PH
                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                                                                                        EMBL; Z98595; CAB11190.1; -. GeneDB_SPombe; SPAC11E3.11c; -.
                                                                                                                                                                                      Submitted
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                      InterPro; IPR001849; PH.
InterPro; IPR000904; Sec7.
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                               PS50003; PH DOMAIN; 1. PS50190; SEC7; 1.
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                      AA:
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EMBLrel. 06,
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                      105909 MW;
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Pred. No.
                                                                                                                             DOMAIN
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                      A677CE2E619ECDF4 CRC64;
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Length 942;
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Best Local :
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Q9SL18;
01-MAY-2000
                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embry.
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
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01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                      Mutator-like transposase.
STRAIN=cv. Columbia;
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                     AT2G05490
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Last annotation update)
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Best Local
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                                                                                                                      Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bownan C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis"
                    -!- PATHWAY: RESPIRATORY CHAIN; TERMINAL STE-
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE
INNER MEMBRANE
-!- SIMILARITY: BELONGS TO THE HEME-COPPER F
EMBL; AF242032; AAK66961.1; --
InterPro; IPR0000883; COX1.
Pfam; PF00115; COX1; 1.
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 22, Last annotation update)
Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxi
                                                                                                                                                                                                                                                                                                                                                                                                     Q955K1;
01-DEC-2001
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 Oxidoreductase; Respiratory
                                                                                                                                                                                                                                                STRAIN-MMT4;
                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                     Mitochondrion.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Q955K1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV.
                                                                                                                                                                                                                                                                              NCBI_TaxID=6551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
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STRAIN=cv. Columbia;
                                                                                                                                                                                                                                                                                                                                                     Fragment)
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                                                                                                      CATALYTIC ACTIVITY: 4
C + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF03108; MuDR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR006564; Znf_PMZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               942 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67
            transport;
                                                                                                                                                                                                                                                                                                                               (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106737 MW;
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                                                                                                                   FERROCYTOCHROME
Heme;
chain;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ODE83F5F5AC0B71E
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Inner membrane;
; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                             57
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                                                                                             STEP
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                                                         RESPIRATORY
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Membrane;
Transport;
                                                                                                                   11
                                                                                MITOCHONDRIAL
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                                                         OXIDASE FAMILY
                                                                                                                   FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                                               RESPIRATORY
SUBUNITS 1-
IS THE
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RESULT 10
Q8LXS2
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DA E
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Best Local
                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                       Matches
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NON_TER 5
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                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MI
INNER MEMBRANE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riginos C., Hickerson M.J., Henzler C.M., Cunningham C.W.; Riginos C., Hickerson M.J., Henzler C.M., Cunningham C.W.; A multilocus study of differential patterns of male and fem. Atlantic gene flow in the blue mussel, Mytilus edulis."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RICHAIN THAT CATTALYZES THE REDUCTION OF OXYGEN TO WATER. SI PORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IL CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IL CATALYTIC SUBUNIT OR THE COPPER A CENTER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Moi
Mytiloidea; Mytilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8LXR7
Q8LXS2;
01-OCT-2002 (TrEMBLrel.
                           Q8LXS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=759NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mytilus trossulus
                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                    Oxidoreductase; Respiratory
                                                                                                                                                                                                                                                                                                                            EMBL; AY101434; AAM63589.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=6551;
                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: RESPIRATORY CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                          AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC AND COPPER B (BY SIMILARITY).
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                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                  Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                   PR01165; CYCOXIDASEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STMLS
                                                                                                 SYWLS
                                                                                                                            SYMMS 5
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                                                                                                                                                                                                                                                                                                              IPR000883;
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                                                                                                                                                        Conservative
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                           PRELIMINARY;
                                                                                                                                                                                                                            89
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                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVITY: 4
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                                                                                                 22
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                                                                                                                                                                                                                              89
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80.0%;
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                                                                                                                                                                                                                MW.
22,
                                                                                                                                                                                                                                                                                                                                                                                                               FERROCYTOCHROME
                                                                                                                                                                                                                                                                       chain;
                                                                                                                                                                                                                                                                                    Heme;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    370D7C4075ADEA71
                                                                                                                                                                       Score 28; I
Pred. No. 3
                                                                                                                                                                                                                85CA357AE7D8F8C4
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                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                     Inner membrane;
Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CENTER
                                                                                                                                                                                                                CRC64;
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                                                                                                                                                                                                                                                                       Membrane;
Transport;
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                                                                                                                                                                                                                                                                                                                                                                                                                 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IS THE
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SUBUNITS 1-
                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT
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"A multilocus study of differential patterns of male and female
"A multilocus study of differential patterns of male and female
"A tlantic gene flow in the blue mussel, Mytilus edulis.";

"A transition of the blue mussel, Mytilus edulis.";

"A tlantic gene flow in the blue mussel, Mytilus edulis.";

"A transition of the mussel, Dublis edulis.";

"A transition of the EMBL/General THE COMPONENT OF THE RESP.

"A THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE CATALYTIC SUBUNIT OF THE ENZYME, ELECTRONS ORIGINATING IN CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF SUBLAND COPPER B (BY SIMILARTIY).

"A multilocus study of differential patterns."

"A multilocus differential patterns."

"A mu
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Best Local
                                                                                                                                                                                                                                                                                                                                         Q8LXS3;
Q8LXS3;
01-OCT-2002
01-OCT-2002
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AY101412; AAM63567.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PATHWAY: RESPIRATORY CHAIN; TEI
-!- SUBCELLULAR LOCATION: INTEGRAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mytiloidea; Mytilidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mytilus edulis
 Riginos C., Hickerson M.J., Henzler C.M., Cunningham C.W.; manultilocus study of differential patterns of male and fe atlantic gene flow in the blue mussel, Mytilus edulis."; Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER.
                                                                                                                                                                                     Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                Micochondrion
                                                                                                                                                                                                                                                 Mytilus edulis
                                                                                                                                                                                                                                                                                                                         01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS;
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                                                                                                                 STRAIN=366ME;
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                    (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INNER MEMBRANE (BY SIMILARITY) SIMILARITY: BELONGS TO THE HEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SYMMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR01165; CYCOXIDASEI.
                                                                                                                                  FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYWLS 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
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                                                                                                                                                                                                                                                                                                      oxidase
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(TrEMBLrel. 22, Last
(TrEMBLrel. 23, Last
(TrEMBLrel. 23, Last)
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                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                 (Blue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Blue mussel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mollusca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11372
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                                                                                                                                                                                                                                                   mussel).
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Last annotation update)
9.3.1) (Cytochrome c oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heme;
chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28; DB Pred. No. 3.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEME-COPPER RESPIRATORY OXIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13F4DAF375E5AE73 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TERMINAL STEP
RAL MEMBRANE PI
                                                                                                                                                                                                                                                                                                                         annotation update)
                                                                                                                                                                                                                                                                                                                                           sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inner membrane;
; Transmembrane;
                                                                                                                                                                                                                                                                                                          (Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                       107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 8;
3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oxidase
                                                                                                                                                                                                                                                                                                            oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 = 4 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide
                                                                                                                                                                                                                                                                                                          polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          female trans-
                                                                               female trans-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
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BY HEME
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     RESPIRATORY
SUBUNITS 1-
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                                                                                                                                                                                                                                                                                                            H)
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3 FORM THE CATALYTIC SI CYTOCHROME AND HEME A

3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED AND COPPER B (BY SIMILARITY).

CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 4 FERE

-!- SIMILARITY: BELONGS TO THE EMBL; AY101407; AAM63562.1; -.

HEME-COPPER RESPIRATORY OXIDASE FAMILY

0

SUBCELLULAR LOCATION: INTEGRAL INNER MEMBRANE (BY SIMILARITY). PATHWAY: RESPIRATORY CHAIN;

TERMINAL

MEMBRANE

ANE PROTEIN.

MITOCHONDRIAL

4 FERRICYTOCHROME

FORMED

ဝ္ဗ

SUBUNIT BY HEME

A3 2

NI SI

HH

+ 2 H(2)

PRINTS; InterPro;

PR01165; CYCOXIDASEI.

IPR000883; COX1.

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RESULT 12
Q8LXS0
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Best Local S
Matches 4
                                                                -I- SUBCELLULAR LOCATION: INTEGRAL INNER MEMBRANE (BY SIMILARITY)
-I- SIMILARITY: BELONGS TO THE HEW EMBL; AX101420; AAM63575.1; -.
InterPro; IPR000883; COX1.
                                                                                                                                                                                                                                     Riginos C., Hickerson M.J., Henzler C.M., Cunningham C.W. "A multilocus study of differential patterns of male and Atlantic gene flow in the blue mussel, Wytilus edulis.", Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                          Riginos C., Hickerson M.J., Henzler C.M., "A multilocus study of differential patter
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mol
Mytiloidea; Mytilidae;
                                                                                                                                                                                                                                                                                                                                                                                                Cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oxidoreductase; Respiratory chain;
           Mitochondrion.
                               Copper; Electron transport; Heme; Inner membrane; Oxidoreductase; Respiratory chain; Transmembrane;
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                     Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                               Mytilus edulis
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8LXS0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTX20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                    (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TER
                                                                                                              PATHWAY: RESPIRATORY CHAIN; TERMINAL SUBCELLULAR LOCATION: INTEGRAL MEMBRI
                                                                                                                                                                                                   FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I
                                                                                                                                                CATALYTIC
                                                                                                                                                       CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING I CYTOCHROME C ARE TRANSFERRED VIA THE COPPER A CENTER OF AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED AND COPPER B (BY SIMILARITY).
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                                                    PR01165; CYCOXIDASEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMMAS
                                                                                                                                    H(2)
                                                                                                                                                                                                                                                                                                                                                                                               oxidase I (EC
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                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
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 108
                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                               ACTIVITY: 4 FERROCYTOCHROME
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                                                                                                                                                                                                                                                                                                                                                               (Blue mussel).
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11598 MW;
108
                                                                                                                                                                                                                                                                                                                                         Mollusca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.3%;
                                                                                                                                                                                                                                                                                                                              Mytilus
                                                                                                                                                                                                                                                                                                                                                                                              22, Created)
22, Last sequence update)
23, Last annotation update)
C 1.9.3.1) (Cytochrome c oxidase polypeptide I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28; DB
Pred. No. 4e+0
1; Mismatches
                                                                                                                                                                                                                                                                                                                                         Bivalvia;
                                                                                        HEME-COPPER RESPIRATORY OXIDASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5E6104D10C023051 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                              MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                         Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                         STEP
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+
                                                                                                             PROTEIN. MITOCHONDRIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 107;
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                               Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane;
                                                                                                                                               11
                                                                                                                                              4.
                                                                                                                                              FERRICYTOCHROME
                                                                                                                                                                                                                                                            female
                                                                                                                                                                                                                RESPIRATORY
SUBUNITS 1-
                                                                                                                                                                                          i is
                                                                                                                                                                    SUBUNIT
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Cytochrome

oxidase

? (TrEMBLrel. 22, 0 2 (TrEMBLrel. 22, 1 3 (TrEMBLrel. 23, 1 0xidase subunit I

Last I (EC

sequence update)
annotation update)
1.9.3.1) (Cytochrome

a

oxidase

Created)

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RESULT 13
Q8LXS1
ID Q8LXS
RESULT 14
Q8LXA4
ID Q8LXA
AC Q8LXA
DT 01-OC
DT 01-OC
DT 01-MA
DE Cytoo
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Matches 4
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Best Local
           Q8LXA4
Q8LXA4;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                      Riginos C., Hickerson M.J., Henzler C.M., Cunningham C.W.;
Riginos C., Hickerson M.J., Henzler Soft male and fem
Atlantic gene flow in the blue mussel, Mytilus edulis.";
Submitted (MAY-2002) to the EMELYGENANK/DDBJ databases.
-i- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE R.
-i- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE R.
-i- FUNCTION: CONTROL OF THE EMEXYME COMPLEX. CO I I
CATALYTIC SUBUNIT OTHE BIMETALLIC CENTER FORMED
AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER FORMED
                                                                                                                                                                                                                                                                    Copper; Electron transport; Oxidoreductase; Respiratory
                                                                                                                                                                                                                                                                                                                                                                      AND HEME A OF SUBUNIT 1 TO THE BIMETALLIC CENTER AND COPPER B (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = C + 2 H(2)O.

-I- PATHWAY: RESPIRATORY CHAIN; TERMINAL STEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Mo. Mytiloidea; Mytiloidea; Mytilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Cytochrome oxidase I (EC 1.9.3.1) (Cytochrome c oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                      EMBL; AY101417; AAM63572.1; -.
                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: INTEGRAL INNER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8LXS1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8LXS1
                                                                                                                                                                                                                                                            Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=A.WH10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mytilus edulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Fragment).
                                                                                                                       18
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                                                                                                                                                                                    Similarity
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                                                                                                                       SYWLS
                                                                                                                                                SMMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYWLS
                                                                                                                                                                                                                                                                                                             IPR000883; COX1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
                                                                                                                                                                                                                       108 AA;
                                                                                                                                                                                                                                     108
                                                                                                                                                                       Conservative
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                                                            PRELIMINARY;
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                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                        11712 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11680
                                                                                                                                                                                    90.3%;
80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WW;
                                                                                                                                                                                                                                                                                                                                                             INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                        Heme;
chain;
                                                                                                                                                                        1;
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                                                                                                                                                                                    Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                      HEME-COPPER RESPIRATORY OXIDASE FAMILY
                                                                                                                                                                                                                         28D7C826D3297545 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28D7CD8208416745 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                        Mismatches
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Transmembrane; Transport;
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                                                            108
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                                                                                                                                                                                    DB 8;
4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                  4 FERRICYTOCHROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          v.;
d female
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IS THE
IN
                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT
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QBLXR
QBLXR
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DT 01-MA
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DE (Frag
GN COI.
OS MYtil
OS MYtil
OS MYtil
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RR (1)
RR (2)
RR (3)
RR (1)
RR (1)
RA mu
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RT SEQUE
RT Atlan
RT SUDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                       Q8LXR9;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN=G.FM99.1;

Riginos C., Hickerson M.J., Henzler C.M., Cunningham C.W.;

Riginos C., Hickerson M.J., Henzler Soft male and female trans-

Atlantic gene flow in the blue mussel, Mytilus edulis.";

Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: CYTOCHROME COXIDASE IS THE COMPONENT TO WATER. SUBUNITS 1-

3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. CO I IS THE

CATALYTIC SUBUNIT OF THE ENZYME. ELECTRONS ORIGINATING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide I) (Fragment).
COI.
Mytilus edulis (Blue mussel).
Mitochondrion.
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=E.NC3;
                                                                                                                                                                                                                     Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                     Mitochondrion.
                                                                                                                                                                                                                                                                      Mytilus edulis (Blue mussel).
                                                                                                                                                                                                                                                                                                                       Cytochrome oxidase
                                                                                                                                                                                                                                                                                                                                                                                                            Q8LXR9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Respiratory chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000883; COX1.
PRINTS; PR01165; CYCOXIDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AY130035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=6550;
                                                                                                                                                                                                      NCBI_TaxID=6550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitochondrion.
                                                                                                                                                                                                                                                                                                      (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C + 2 H(2)O.
PATHWAY: RESPIRATORY CHAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INNER MEMBRANE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Electron transport; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR01165; CYCOXIDASEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STWIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYMMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108 AA;
                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
oxidase I (EC 1.9.3.1) (Cytochrome c oxi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.3%;
ilarity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM83431.1; -.
   ARE TRANSFERRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11762 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN; TERMINAL STEP.
INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB
Pred. No. 4e+(
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68FC2E0C9337D118 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                             108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                             B
   COPPER A CENTER OF SUBUNIT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 108;
                                                                                                                                                                                                                                                                                                                           oxidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transport
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                                                                                                                                                                                                                                                                                                                       polypeptide
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                                                                     Best Loc
Matches
                                                                                          Query Match
                                                                                                              NON TER
NON TER
SEQUENCE
                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE HEME-COPPER RESPIRATORY OXIDASE FAMILY.
EMBL; AY101425; AAM63580.1; -.
                                                                                                                                                                                                                           AND HEME A OF SUBURLL 1 L. AND COPPER B (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C
C + 2 H(2)O.
-I- PATHWAY: RESPIRATORY CHAIN; TERMINAL STE
                                                                                                                                                      Oxidoreductase;
                                                                                                                                                                 PRINTS; PR01165; CYCOXIDASEI. Copper; Electron transport; H
                                                                                                                                             Mitochondrion.
                                                                                                                                                                                      InterPro;
                                                                                Local
                              18
                                                1 SYWMS
                                                                     Similarity 80.4
4; Conservative
                              SYWLS
                                                                                                                                                                                      IPR000883;
                                                                                                               108
                                                                                                                        108
                                                                                                                                                                                                                                                          A OF SUBUNIT 1 TO THE BIMETALLIC CENTER B (BY SIMILARITY).
ACTIVITY: 4 FERROCYTOCHROME C + O(2) =
                                                                                                               AΑ;
                               22
                                                 տ
                                                                                                                                                      Respiratory
                                                                                                              108
11669
                                                                                 90.3%;
12,
2004,
                                                                                                                MW.
                                                                                                                                                       Heme;
chain;
                                                                                 Score
Pred.
 07:01:54
                                                                                                                39C6DF8119537545 CRC64;
                                                                       Mismatches
                                                                                                                                                        Inner membrane;
; Transmembrane;
                                                                                 28;
No.
                                                                                  4e+02;
                                                                                            BB
                                                                                                                                                                                                                               STEP.
NE PROTEIN.
                                                                                           8
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                                                                                            Length 108
                                                                                                                                                       Membrane;
Transport;
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4
                                                                                                                                                                                                                                                                                  FORMED
                                                                                                                                                                                                                                                              FERRICYTOCHROME
                                                                        0
                                                                                                                                                                                                                                                                                  BY HEME A3
                                                                        Gaps
                                                                         0
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Search completed: January Job time: 15.1562 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-829-495-66
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       January 12, 2004, 07:02:25; Search time 16 Seconds (without alignments)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         747907 seqs, 201509753 residues
                                                                                                 10:
11:
12:
13:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maximum Match 100%
Listing first 45 summaries
                /cgn2 6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9_NEW_PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9 NEW_PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9 NEW_PUB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9 PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9B_PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
/cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
2 /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
3 /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
3 /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
3 /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
3 /cgn2 6/ptodata/1/pubpaa/USO9E_PUBCOMB.pep:*
4 /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
5 /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
6 /cgn2 6/ptodata/1/pubpaa/USOB_PUBCOMB.pep:*
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_6/ptodata/1/pubpaa/US10_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.755 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

15	14	13	12	11	10	9	80	7	6	ъ	4	ω	2	L	Result No.
31	31	31	31	32	32	32	32	32	32	32	33	39	39	39	Score
79.5	79.5	79.5	79.5	82.1	82.1	82.1	82.1	82.1	82.1	82.1	84.6	100.0	100.0	100.0	Query
217	103	98	10	4327	1938	893	395	363	174	166	617	161	8	89	Query Match Length DB
11	11	12	11	12	14	14	11	11	11	11	15	15	12	9	BG
US-09-972-656-88	US-09-972-656-130	US-10-308-817-117	US-09-972-656-23	US-10-369-493-10178	US-10-014-436-2	US-10-014-436-4	US-09-797-464A-2	US-09-797-464A-11	US-09-797-464A-9	US-09-797-464A-5	US-10-205-342-11	US-10-106-698-6785	US-09-829-495-66	US-09-832-312-66	ID
Sequence 88, Appl	Sequence 130, App	Sequence 117, App	Sequence 23, Appl	Sequence 10178, A	Sequence 2, Appli	Sequence 4, Appli	Sequence 2, Appli	Sequence 11, Appl	Sequence 9, Appli	Sequence 5, Appli	Sequence 11, Appl	Sequence 6785, Ap		Sequence 66, Appl	Description

ALIGNMENTS

RESULT 1 US-09-832-312-66

0;

Publication No. US20040001826A1

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CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR PILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PATENTIN Ver. 3.0
SEQ ID NO 6785
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US-09-829-495-66
                                                                                                                                                        US-10-106-698-6785
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SEQ ID NO 66
LENGTH: 8
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                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6785, Application US/10106698 Publication No. US20030109690A1 GENERAL INFORMATION:
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Matches 8; Conserv
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                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GLYCOPROTEIN VI AND USES FILE REFERENCE: 7853-234 CURRENT PEPLICATION NUMBER: US/09/829,495 CURRENT FILING DATE: 2001-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jandrot-Perrus M
APPLICANT: Vainchenker W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Busfield SJ
                                                                                                                                                                                           FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (149)
                                                                                                                                                                                                                                                                             LENGTH: 161
TYPE: PRT
                                                                                                                                                                           OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino
                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
  114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SYDSSNVV 8
                                      1 SYDSSNVV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FastSEQ for Windows Version
SYDSSNVV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AANSSUAS
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Qian MD
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                                                                         100.0%; Score 39; DB 15; Length 161; ilarity 100.0%; Pred. No. 3.5; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Pred. No. 6.6e+05;
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Sequence 11, Application US/10205342
Publication No. US20030108906A1
GENERAL INFORMATION:
APPLICANT: Warner-Lambert Company
APPLICANT: Lee, Kevin
APPLICANT: Lee, Kevin
APPLICANT: Dixon, Alistair
APPLICANT: Dixon, Alistair
APPLICANT: Pinnock, Robert
TITLE OF INVENTION: Identification and Use of Mol
FILE REFERENCE: WL-A-018198
CURRENT APPLICATION NUMBER: US/10/205,342
PRIOR APPLICATION NUMBER: US/10/205,342
PRIOR APPLICATION NUMBER: 3002-07-24
PRIOR APPLICATION NUMBER: US/10/205,342
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
US-10-205-342-11
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                                                                                                                                                                    US-09-797-464A-5
                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 166
TYPE: PRT
ORGANISM: Paenibacillus pabuli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.0 SEQ ID NO 11 LENGTH: 617
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                                                                                  Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/09797464A Publication No. US20030022807A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wilting, Reinhard
APPLICANT: Bjornvad, Mads Eskelund
APPLICANT: Kauppinen, Markus Sakari
APPLICANT: Schulein, Martin
TITLE OF INVENTION: Family 5 Xyloglucanases
FILE REFERENCE: 6073.200-US
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/797,464A
CURRENT FILING DATE: 2002-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: Protein: vacuolar adenosine triphosphatase subunit A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
108 SYDSSNNV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 NYDASNVV 191
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                                       1 SYDSSNVV 8
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                                                                                  Conservative
                                                                                                      82.1%;
87.5%;
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75.0%;
                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                        Score 32;
Pred. No.
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Pred. No. 2.2e+02;
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                                                                                      Mismatches
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RESULT 6 US-09-797-464A-9

Sequence 9, Application US/09797464A publication No. US20030022807A1 GENERAL INFORMATION:
APPLICANT: Wilting, Reinhard APPLICANT: Bjornvad, Mads Eskelund

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Best Local Similarity
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SEQ ID NO 11
LENGTH: 363
TYPE: PRT
ORGANISM: Paenibacillus pabuli
                                                CURRENT APPLICATION NUMBER: US/09/797,464A
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 395
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Best Local Similarity
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LENGTH: 174
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Publication No. US20030022807A1
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TYPE: PRT ORGANISM: Paenibacillus pabuli -09-797-464A-2
                                                                                                                                                    APPLICANT: Bjornvad, Mads Eskelund APPLICANT: Kauppinen, Markus Sakari APPLICANT: Schulein, Martin TITLE OF INVENTION: Family 5 Xyloglucanases FILE REFERENCE: 6073.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/797,464A
CURRENT FILING DATE: 2002-02-19
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Family 5
FILE REFERENCE: 6073.200-US
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APPLICANT: Bjornvad, Mads E
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ORGANISM: Paenibacillus pabuli
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PPLICANT: Schulein, Martin
TTLE OF INVENTION: Family 5 Xyloglucanases
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87.5%;
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Pred. No.
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Best Local Similarity
"htches 7; Conserve
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APPLICANT: ITO, SUBUMU
TITLE OF INVENTION: Gene for Enzyme Having Bo
TITLE OF INVENTION: Amylase Activites
FILE REFERENCE: 2173-0122P
CURRENT APPLICATION NUMBER: US/10/014,436
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: JP 111547/1995
PRIOR FILING DATE: 1995-05-10
PRIOR APPLICATION NUMBER: BCT/JP96/01243
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR APPLICATION NUMBER: US 08/952,084
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Best Local Similarity
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PRIOR APPLICATION NUMBER: US 08/952,084
PRIOR PILING DATE: 1997-11-10
PRIOR APPLICATION NUMBER: US 09/514,302
PRIOR FILING DATE: 2000-02-28
                                                                                                                                                                                                                                                                                                       APPLICANT: HATADA,
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PRIOR APPLICATION NUMBER: PCT/JP96/01243
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CURRENT FILING DATE: 2002-05-21
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TITLE OF INVENTION: Gene for Enzyme Having
TITLE OF INVENTION: Amylase Activites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HATADA, Yuji
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ORGANISM: Bacillus sp
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IGARASHI, Nu.
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ARA, Katsutoshi
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IGARASHI, Kazuaki
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62.5%;
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Pred. No. 5e+02;
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Pred. No. 2.1e+02;
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RESULT 12
US-09-972-656-23
US-09-972-656-23
, Sequence 23, Application US/09972656
, Publication No. US20030099647A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
                              CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
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LENGTH: 4327
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Publication No. US20030233675A1
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Best Local Similarity
Matches 5; Conserv
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Matches 6; Conserv
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TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 39-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                     TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma TITLE OF INVENTION: Neutralizing Activity FILE REFERENCE: A-799
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
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                                                                                                                                                                                              APPLICANT: Deshpande, Rajendra APPLICANT: Tsai, Mei-Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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ORGANISM: Bacillus sp
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LOCATION: (1)...(4327)
OTHER INFORMATION: unsure at all Xaa locations
LENGTH: 10
TYPE: PRT
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62.5%;
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Pred. No. 2.7e+03;
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Pred. No. 1.1e+03;
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US-10-308-817-117
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US-09-972-656-130
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LENGTH: 98
TYPE: PRT
ORGANISM: human
                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin version 3.0
SEQ ID NO 130
LENGTH: 103
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Publication No. US20030219861A1
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Matches 6; Conserv
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CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Fully Human Antibody Fab Pragments with Human Interferon-Gamma TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Deshpande, Rajendra APPLICANT: Tsai, Mei-Mei
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APPLICANT: Wu, Dayang
TITLE OF INVESTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
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OTHER INFORMATION: Unidentified
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LOCATION: (33)..(33)
                                                                                                                                                                                         NAME/KEY: Misc.
LOCATION: (7)..(7)
OTHER INFORMATION: Unidentified
                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                             OTHER INFORMATION: Unidentified
                                                                NAME/KEY: Misc.
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100.0%;
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Pred. No.
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RESULT 15
US-09-972-656-88
US-09-972-656-88
; Sequence 88, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
: APPLICANT: Deshipande, Rajendra
: APPLICANT: Deshipande, Rajendra
: APPLICANT: Teal, Mei-Mei
: TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
: TITLE OF INVENTION: Neutralizing Activity
: FILE REFERENCE: A-799
: CURRENT APPLICATION NUMBER: US/09/972,656
: CURRENT FILING DATE: 2001-10-05
: NUMBER OF SEQ ID NOS: 135
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 88
: LENGTH: 217
: TYPE: PRT
: ORGANISM: Homo sapiens

US-09-972-656-88
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Search completed: January 12, 2004, 07:19:58 Job time : 18 secs
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Listing first 45 summaries
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29 74.4 469 3 US-09-832-441-2 Sequence 3, A; 29 74.4 599 4 US-09-832-102-2 Sequence 2, A; 29 74.4 600 2 US-08-679-405-2 Sequence 2, A; 29 74.4 600 2 US-08-679-405-2 Sequence 2, A; 29 74.4 600 3 US-09-718-718-2 Sequence 2, A; 29 74.4 600 4 US-09-718-871-2 Sequence 2, A; 29 74.4 600 4 US-09-718-871-2 Sequence 2, A;	29 74.4 40 5 PCT-US96-11458-6 Sequence 6, Ag. 29 74.4 109 3 US-09-157-370-5 Sequence 3.07, 29 74.4 129 4 US-09-615-192A-307 Sequence 307, 29 74.4 357 4 US-09-252-991A-24337 Sequence 24337 29 74.4 469 3 US-08-378-431-3 Sequence 23.4, 469 4 US-09-832-441-2 Sequence 2, Ag. 29 74.4 599 4 US-09-833-102-2 Sequence 2, Ag. 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ag. 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ag. 29 74.4 600 3 US-09-271-778-2 Sequence 2, Ag. 29 74.4 600 3 US-09-271-778-2 Sequence 2, Ag. 29 74.4 600 3 US-09-271-778-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2	29 74.4 40 2 US-08-842-799-6 Sequence 6, Ag. 29 74.4 40 5 PCT-US96-11458-6 Sequence 6, Ag. 29 74.4 109 3 US-09-157-370-5 Sequence 5, Ag. 29 74.4 109 3 US-09-157-370-5 Sequence 5, Ag. 29 74.4 129 4 US-09-615-192A-307 Sequence 307, 29 74.4 357 4 US-09-252-991A-24337 Sequence 24333 29 74.4 469 3 US-09-378-313 Sequence 23, Ag. 29 74.4 599 4 US-09-832-141-2 Sequence 2, Ag. 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ag. 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ag. 29 74.4 600 3 US-08-871-78-2 Sequence 2, Ag. 29 74.4 600 3 US-09-271-778-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2	29 74.4 40 2 US-08-679-405-6 Sequence 6, Ag. 29 74.4 40 2 US-08-842-799-6 Sequence 6, Ag. 29 74.4 40 5 PCT-US96-11458-6 Sequence 6, Ag. 29 74.4 109 3 US-09-157-370-5 Sequence 5, Ag. 29 74.4 1109 3 US-09-157-370-5 Sequence 5, Ag. 29 74.4 129 4 US-09-252-991A-24337 Sequence 20, Ag. 29 74.4 469 3 US-08-378-313-33 Sequence 23, Ag. 29 74.4 469 3 US-08-378-313-33 Sequence 23, Ag. 29 74.4 599 4 US-09-833-141-2 Sequence 2, Ag. 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ag. 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ag. 29 74.4 600 3 US-09-271-778-2 Sequence 2, Ag. 29 74.4 600 3 US-09-788-871-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2 Sequence 2, Ag. 29 74.4 600 4 US-09-788-871-2	29 74.4 25 6 5248606-16 29 74.4 40 2 US-08-679-405-6 29 74.4 40 2 US-08-842-799-6 29 74.4 40 2 US-08-842-799-6 29 74.4 40 5 PCT-US96-11458-6 29 74.4 109 3 US-09-157-370-5 29 74.4 129 4 US-09-615-192A-307 29 74.4 129 4 US-09-615-192A-307 29 74.4 469 3 US-09-813-3337 Sequence 307, 207, 207, 207, 207, 207, 207, 207, 2	29 74.4 25 1 US-08-485-286-30 Sequence 30.7 29 74.4 25 6 5248606-16 29 74.4 40 2 US-08-679-405-6 Sequence 6, Ap. 29 74.4 40 2 US-08-842-799-6 Sequence 6, Ap. 29 74.4 40 5 PCT-US96-111458-6 Sequence 6, Ap. 29 74.4 109 3 US-09-157-370-5 Sequence 30.7 29 74.4 129 4 US-09-615-192A-307 Sequence 20.7 29 74.4 357 4 US-09-6252-991A-24337 Sequence 20.7 29 74.4 599 4 US-09-832-441-2 Sequence 30.7 29 74.4 599 4 US-09-832-441-2 Sequence 2. Ap. 29 74.4 600 2 US-08-679-405-2 Sequence 2. Ap. 29 74.4 600 3 US-08-679-405-2 Sequence 2. Ap. 29 74.4 600 3 US-09-788-871-2 Sequence 2. Ap. 29 74.4 600 4 US-09-788-871-2	29 74.4 25 1 US-08-378-761A-30 Sequence 30, # 29 74.4 25 1 US-08-485-286-30 Sequence 30, # 29 74.4 25 6 5248606-16 29 74.4 40 2 US-08-679-405-6 Sequence 6, Ap 29 74.4 40 2 US-08-842-799-6 Sequence 6, Ap 29 74.4 40 5 PCT-US96-111458-6 Sequence 6, Ap 29 74.4 40 5 PCT-US96-111458-6 Sequence 6, Ap 29 74.4 109 3 US-09-615-192A-307 Sequence 5, Ap 29 74.4 109 4 US-09-615-192A-307 Sequence 307, Ap 29 74.4 469 3 US-09-252-991A-24337 Sequence 33, # 29 74.4 469 3 US-09-833-102-2 Sequence 2, Ap 29 74.4 599 4 US-09-833-102-2 Sequence 2, Ap 29 74.4 600 2 US-08-679-405-2 Sequence 2, Ap 29 74.4 600 3 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 3 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 3 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 4 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 3 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 3 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 3 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 4 US-09-718-718-2 Sequence 2, Ap 29 74.4 600 5 US-08-871-2	29 74.4 16 2 US-08-932-976-1 29 74.4 25 1 US-08-932-976-1 29 74.4 25 1 US-08-302-976-30 Sequence 30, \$\begin{align*} Z \ Z \ Z \ Z \ Z \ Z \ Z \ Z \ Z \ Z	30 76.9 1189 4 US-08-851-567B-26 Sequence 26, A 29 74.4 16 2 US-08-332-876-1 Sequence 30, A 29 74.4 25 1 US-08-378-761A-30 Sequence 30, A 29 74.4 25 1 US-08-485-286-30 Sequence 30, A 29 74.4 25 6 5248606-16 Patent No. 5248 29 74.4 40 2 US-08-879-405-6 Sequence 6, A 29 74.4 40 2 US-08-842-799-6 Sequence 6, A 29 74.4 10 3 US-09-157-370-5 Sequence 6, A 29 74.4 10 3 US-09-157-370-5 Sequence 5, A 29 74.4 129 4 US-09-615-192A-307 Sequence 307, A 29 74.4 357 4 US-09-615-192A-307 Sequence 24337 29 74.4 460 3 US-09-832-412-2 Sequence 33, A 29 74.4 599 4 US-09-832-102-2 Sequence 2, A 29 74.4 600 2 US-08-879-405-2 Sequence 2, A 29 74.4 600 3 US-09-271-778-2 Sequence 2, A 29 74.4 600 4 US-09-788-871-2

ALIGNMENTS

RESULT 1 US-09-832-312-66

Sequence 66, Application US/09832312 Patent No. 6548741

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US-09-107-532A-5317
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CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR APPLICATION NUMBER: 09/345,468
                                                                                                                                   Sequence 5317, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version SEQ ID NO 66
LENGTH: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                          NUMBER OF SEQUENCES: 73.
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME
                                                                                                                                                                                                                                                                                                                                                               1 SYDSSNVV 8
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                                                                                                                                                                                                                                                                                                                                         SYDSSNVV
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                   7310
                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 4;
Pred. No. 2.5e+05;
Mismatches 0;
                                                                                                                                       and David Bush
AND AMINO ACID SEQUENCES RELATING
FAECIUM FOR DIAGNOSTICS AND THERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                         AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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COMPUTER

JTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC

OPERATING SYSTEM: <Unknown>

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CURRENT APPLICATION NUMBER: US/09/514,302
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: 08/952,084
; EARLIER FILING DATE: 1997-11-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 893
; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-514-302-4
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LOCATION: (B) LOCATION 1...515
SEQUENCE DESCRIPTION: SEQ ID NO: 5317:
US-09-107-532A-5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-514-302-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local &
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Applic Patent No. 6338959
                                                                                                                                                                                                                                                                                             APPLICANT: OZAKI, KATBUYA
APPLICANT: KAWAI, KATBUYOSHI
APPLICANT: KAWAI, Shuji
APPLICANT: ITO, SEUSUMU
TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PULLULANASE AND
TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE ACTIVITIES
FILE REFERENCE: 2173-105P
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HATADA, Yuji
APPLICANT: IGARASHI, Ka:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5317:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION NUMBER: 60/085,598

PRIOR APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: 101y 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariniello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REGERENCE/DOCKET NUMBER: GTC-012

TELEPHONE: (781)893-5007

TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 AYDSSNV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 SYDSSNV 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09514302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kazuaki
82.1%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 4;
Pred. No. 1.4e+02;
1; Mismatches 0
Score 32; DB 4;
Pred. No. 2.6e+02;
                    Length 893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 515;
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; TYPE: PRT
; ORGANISM: Bacillus sp.
US-09-514-302-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-869-933-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: GENE FOR ENZYME HAVING BOTH ALKALINE PULLULANASE AND TITLE OF INVENTION: ALKALINE ALPHA-AMYLASE ACTIVITIES FILE REFERENCE: 2173-105P CURRENT APPLICATION NUMBER: US/09/514,302 CURRENT FILING DATE: 2000-02-28 EARLIER APPLICATION NUMBER: 08/952,084 EARLIER APPLICATION NUMBER: 08/952,084 EARLIER FILING DATE: 1997-11-10 NUMBER OF SEQ ID NOS: 14 SOFTWARE: Patentin Ver: 2.1 SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12, Application US/07869933 Patent No. 5770396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 2, Application US/09514302
Patent No. 6338959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 777.

APPLICANT: KINET, Jean-Pierre
APPLICANT: KINET, Jean-Pierre
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
TYPE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
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                                                                                                   COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION MOMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: IGARASHI, Kazuaki
APPLICANT: OZAKI, Katsuya
APPLICANT: ARA, Katsutoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KAWAI, Shuji
APPLICANT: ITO, Susumu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: HATADA,
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 403
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 22313-0299
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                              CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1669 ŚYDŚŚDII 1676
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Pred. No. 6.1e
3; Mismatches
                          40399/154 NIHD
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                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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INFORMATION FOR SEQ ID NO:

12:

899149

TELEFAX:

(703) 683-4109

(703)836-9300

TELEPHONE:

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Query Match
Best Local Similarity
Watches 5; Conserva
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                                                                              US-07-869-933-28
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; STRAIN: FCRI alpha subunit
US-07-869-933-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     atent No. 5770396
GENERAL INFORMATION:
                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 4039
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                    TELEX: 899149
[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: line MOLECULE TYPE: p
                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE: STRAIN: alpha subunit
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                  TELEPHONE: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 19920
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Alexandria
                                                                                                                                                         ENGTH:
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1 SYDSSNV 7
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5; Conserv
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                                                                                         alpha subunit
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                                                                                                                                                                                                                                                                                                                                                           PatentIn
                          Conservative
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71.4%;
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THE HUMAN B SUB
IMMUNOGLOBULIN
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Pred. No.
                          2; Mismatches
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                                       Score 31;
Pred. No.
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B SUBUNIT OF THE H
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90;
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                          <u>.</u>
                                                   Length 222;
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US-08-311-731A-45
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                                                                                                                       RESULT 9
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US-09-103-663-28
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LENGTH: 222
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn
SEQ ID NO 28
LENGTH: 222
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TITLE OF INVENTION: Isol
TITLE OF INVENTION: immu
                                                                   Sequence 45, Application US/08311731A Patent No. 6583266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kinet et al
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Patent No. 6171803
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Best Local
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Patent No. 6171803
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Best Local Similarity
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                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Isolation, characterization, and use of the human beta TITLE OF INVENTION: subunit of the high affinity receptor for TITLE OF INVENTION: immunoglobulin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 50490
APPLICANT: SMITH, DOUGLAS
APPLICANT: MAO, JEN-I
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity es 5; Conserv
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                                                                                                                                                                                                           1 SYDSSNV 7
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Pred. No.
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Pred. No.
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GENERAL INFORMATION:

APPLICANT: De Villiers Zur Hausen, Ethel-Micelle

APPLICANT: Zur Hausen, Harald

TITLE OF INVENTION: PAPILLOMA VIRUS, AGENTS FOR THE DETECTION

TITLE OF INVENTION: THERAPY

TITLE OF INVENTION: OF THE DISEASES CAUSED BY SAID VIRUS

FILLE REFERENCE: 008494-0082-999

CURRENT APPLICATION NUMBER: US/09/485,973

CURRENT FILING DATE: 2001-08-15

PRIOR APPLICATION NUMBER: PCT/DE98/02379

PRIOR APPLICATION NUMBER: DT/DE98/02379

PRIOR APPLICATION NUMBER: 197 35 118.2

PRIOR APPLICATION NUMBER: 197 35 118.2

PRIOR APPLICATION NUMBER: 197-08-13
                                                          ; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Papillomavirus Capsid Protein
US-09-485-973-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-485-973-6
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Matches 6; Conserv
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Patent No. 6488935
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Query Match
Best Local Similarity
                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14
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INFORMATION FOR SEQ ID NO: 45:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GAATES, EDWARD R.
REGISTRATION NUMBER: 31,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PP C COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
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LENGTH: 382 amino acid
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  76.9%;
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75.0%;
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  Score 30;
Pred. No.
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Pred. No. 1.6e+02;
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    DB
76;
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                                                                                                    Sequence 53, Application PC/TUS9601314
GENERAL INFORMATION:
APPLICANT: M. Amin Arnaout
TITLE OF INVENTION: METHODS FOR ID
TITLE OF INVENTION: ANTAGONISTS
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Matches 7; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
APPLICATION UNUMBER: 08/380
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
NAME: John W. Freeman
REGISTRATION NUMBER: 29,06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PS/2 Model 50Z or 55S
OPERATING SYSTEM: MS-DOS (Version 5
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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                                                                       NUMBER OF SEQUENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                           STREET:
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COUNTRY:
                                                            ADDRESSEE:
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                           Boston
              Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 amino acids
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                                             225 Franklin Street
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                                                                                                                                                                                                                                                                                                                Conservative
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IBM PS/2 Model 50Z or 55SX
SYSTEM: MS-DOS (Version 5.0)
                                                            Fish & Richardson P.C
                                                                                                                                                                                                                                                                                                                                                                                                           linear
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87.5%;
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                                                                                                                          METHODS FOR IDENTIFYING INTEGRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08/380,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT/US96/01314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    00786/267001
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                                                                                                                                                                                                                                                                                                                              Score 30; DB 5;
Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
                                                                                                                                                                                                                                                                                                                                             Length 252;
                                                                                                                                                                                                                                                                                                                 Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
COMPUTER: IBM PS/2 Model 50

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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6159469
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILLING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                       COMPUTER: HP Vectra
OPERATING SYSTEM: MS
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 29,066
                                                                   NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                   FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: John W. Freeman
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 SEDSSNVV 245
                                                                                                                                                                                                                                                                                                                                                               20850
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                                                                                                                                                                                                                                                                                                                                                                                               Maryland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                       HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                        Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                        MSDOS version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.9%;
87.5%;
                                                                                                                                                                                                                                  US/08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53:
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Pred. No.
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1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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RESULT 15 US-08-851-567B-28

; Sequence 28, Application US/08851567B

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                                                Query Match
Best Local Similarity
Friches 6; Conserve
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                                                                                                                                US-09-536-784-72
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US-09-536-784-72
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Patent No. 6573082
GENERAL INFORMATION:
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILLING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 72:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Choi et. al. TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines NUMBER OF SEQUENCES: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 SYDSSDAV 370
                                1 SYDSSNVV 8
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SYDSSDAV 370
                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                 LENGTH: 618 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOPTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                               TELEPHONE: (301) 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09536784
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                                                                 Conservative
                                                                               76.9%; Score 30; DB 4; 75.0%; Pred. No. 4.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.9%;
75.0%;
                                                                                                                                                                                                                                                                                   309-8512
                                                                1; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.50 inch, 1.4Mb storage
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                                                                                               Length 618;
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Patent No. 6528484

INFORMATION:

Ensign, Jerald Bowen, David J Petell, James

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COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PStentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/8/851,567B
FILING DATE: 05-WAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION NUMBER: US 60/007,255
FILING DATE: 28-FEB-1995
PRIOR APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1995
PRIOR APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-BEB-1996
PRIOR APPLICATION NUMBER: US 08/705,484
FILING DATE: US 08/705,497
FILING DATE: 
                                                                                                                            Query Match 76.9%; Score 30; DB 4; 1
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 1
                                                                                                                                                                                                                                                                                               TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 627 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                       -08-851-567B-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ciche, Todd A.
APPLICANT: Sukhapinda, Kitisri
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 9330 Zionsv
CITY: Indianapolis
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336 YDSGNVI 342
                                                              2 YDSSNVV 8
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                                                                                                                                                                                                                                                                                                                                                                                                   627 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts, Jean L.
Strickland, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schoonover, Sue
ffrench-Constant, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petell, James
Fatig, Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rocheleau, Thomas A.
Blackburn, Michael B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hey, Timothy D.
Merlo, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lining
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                                                                                                                                   1; Indels
                                                                                                                                                                                                 Length 627;
                                                                                                                                   0;
                                                                                                                                      Gaps
                                                                                                                                      0,
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Search completed: January 12, 2004, 07:04:03 Job time : 7.625 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 m
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB DB
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued_Patents_AA:*
1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    328717 segs, 42310858 residues
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38
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/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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/cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
GenCore version 5.1.6 (c) 1993 - 2004 Compugen
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US-09-157-370-5
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US-09-025-769B-53
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US-09-372-425A-4
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US-09-116-049-5
US-09-116-049-2
US-09-303-268-2
US-09-844-363-2
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US-09-315-372A-10

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US-09-252-991A-27287
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US-08-468-671-16
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                  Sequence 65, Appl
Sequence 16, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 19, Appl
Sequence 5, Appl
Sequence 53, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 54, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 57, Appl
Sequence 58, Appl
Sequence 59, Appl
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US-09-832-312-65
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Result No.

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US-08-211-202-111	US-08-936-165A-466	US-10-060-509-33	US-09-638-715-33	US-08-264-093-19	US-09-328-352-5073	US-09-252-991A-29248	US-09-252-991A-19245	US-09-129-855A-4	US-09-610-833-4	US-09-480-718-4	US-09-247-154-4	US-09-129-855A-4	US-08-954-470-4	US-08-534-975-4	US-08-983-607-31	US-08-983-607-35	US-08-476-349A-91
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
111, App	466, App	33, Appl	33, Appl	19, Appl	5073, Ap	29248, A	19245, A	4, Appli	4, Appli	4, Appli	4, Appli	4, Appli	4, Appli	4, Appli	31, Appl	35, Appl	Tddw 'TK

ALIGNMENTS

Minimum Maximum

Title:

Run on:

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APPLICATION UNMBER: 09/503,387
PRIOR APPLICATION UNMBER: 09/503,387
CURRENT APPLICATION NUMBER: 09/503,312
CURRENT APPLICATION NUMBER: 09/610,118
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR PILING DATE: 2000-02-14
PRIOR PILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR PILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOPTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 65
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Best Local S
Matches 7
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                                                                                                                                                                                               Sequence 16, Application US/08259372A Patent No. 5565354 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                             NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                         APPLICANT: Ostberg, Lars G. TITLE OF INVENTION: PRODUCTION TITLE OF INVENTION: ANTIBODIES
                         CITY:
STATE:
                                                            ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
COUNTRY:
  : San Francisco
3: CA
FRY: USA
                                                                                                                                                                                                                                                                                                                                               1 EDNORPS
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CURRENT APPLICATION DATA:

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION UNDER: US 07/6
PRIOR APPLICATION UNDER: US 07/6
PILING DATE: 27-MAP-100
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELLEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 1 SEQUENCE CHARACTERISTICS: LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                  tent No.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 01 FILING DATE: 31-OCT-1986 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                       NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew.LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 11-MAY-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                             ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/538,796 FILING DATE: 15-JUN-1990
                                                                                      ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 05-SEP-1986
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                                                                                                     COUNTRY:
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                                                                                    94111-3834
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85.7%;
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PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
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Pred. No. 6.4;
   Version #1.30
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                                                                                                                                                                                                                                                                                                                         Patent No. 5977322
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acids
TYPE: amino acids
TOPOLOGY: limit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 1
FILING DATE: 31-OCT-
PRIOR APPLICATION DATA:
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PRIOR APPLICATION NUMBER: US 07/676,036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/259,372
                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLF
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                 APPLICANT: Marks, James DAPPLICANT: Schier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
                          SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           TITLE OF INVENTION: No. 5977322e1
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B9.5%;
Local Similarity 85.7%;
hes 6; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0 FILING DATE: 05-SEP-1986
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                                                                                                                                                              STATE:
                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
FILING DATE:
                                                                                                                                        COUNTRY:
                                                                                                                                                                             CITY:
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               APPLICATION NUMBER:
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                                                                                                                            94111-3834
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                                                                                                                                                                           San Francisco
                                                                                                                                                            California
                                                                                                                                                                                                                                                                                                                                                           Application US/08665202
                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                           Marks, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (415)
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31-OCT-1986
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15-JUN-1990
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13-JUN-1996
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                                                                                                                                                                                                                                                                           No. 5977322el High Affinity Human
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             US/08/665,202
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                                               Version #1.30
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CLASSIFICATION: 424

IOR APPLICATION DATA:
APPLICATION NUMBER: US 6:
FILING DATE: 14-JUN-1995

us 60/000,238

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Best Local Similarity
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                                                                                                                                                                                  CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/315,574
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,202
FILING DATE: 13-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       FILING DATE: 14-JUN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Marks, James D
APPLICANT: Schier, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER OF SEQUENCES:
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-JUN-
IOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94111-4106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                 NAME: Hunter, Tom REGISTRATION NUMBER:
                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
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6512097
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                                                                                                                                          UMBER: US 60/000,250
15-JUN-1995
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                            38,498
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                02307E-061411
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SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acid
                                                                                                                          APPLICATION NUMBER: US 06/925,196
ETLING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
ETLING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
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                   TELEPHONE: (415) 326-
TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ostberg, TITLE OF INVENTION:
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 06/925,196
                                                                                                                                                                                                                                                                                           FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
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PRIOR APPLICATION NUMBER: US 07/871,426
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SEQUENCE CHARACTERISTICS:
                                                                     TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 424
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CITY: San Francisco
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nes 6; Conservative
                                                                                          NAME: Smith, William M. REGISTRATION NUMBER: 30, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
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R SEQ ID NO: 39:
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                                    576-0300
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                                                       326-2400
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PRODUCTION OF HUMAN MONOCLONAL
ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
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                                                                                                                                                                                                                                                                                                                                                                                                             US 07/676,036
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; Pred. No.
                                                                                             11823-50-7
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. 11;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-259-372A-10
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; MOLECULE TYPE: protein US-08-468-671-10
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GENERAL INFORMATION:
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Best Local :
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                                                                                             TELEFAX: (415) 576-03
                                                                                                                                                          APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 07/192,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/259,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 326-2400
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APPLICATION NUMBER:
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APPLICATION NUMBER: US 06
FILING DATE: 31-OCT-1986
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MEDIUM TYPE: Floppy disk
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                                                LENGTH:
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                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 11-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
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ZIP: 94111-3834
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                                      amino acids
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                                                                                                            (415) 576-0300
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Pred. No.
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16;
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US-08-765-179B-19
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LENGTH: 192
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Marc J.
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Best Local
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                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: STEIDE
APPLICANT: STEINB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                            FILING DATE: 14-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/02626
FILING DATE: 06-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 25 115.7
                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/765,179B
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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les 6; Conserv
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                  FILING DATE:
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NVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
                                                                                                                                                                                                                                                                                                                             E: Nikaido, Marmelstein, Murray & Oram LLP 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                               STEINBACHER,
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Pred. No.
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Pred. No.
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Query Match
Best Local Similarity
Marches 5; Conserve
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Best Local Similarity
Matches 5; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
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LENGTH: 64 amino acids
                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
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                                                                                                                                                                                                                                                                             NAME: James F. Haley, Jr., Esq. REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                TELEPHONE:
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48 DDNKRPS 54
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amino acid
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                                                                                                                                                                                       108 amino acids
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Moroney, Simon
Plueckthun, Andreas
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Ilag, Vic
                                                       Conservative
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18-AUG-1995
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71.4%;
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Pred. No. 26;
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Pred. No.
                                                        Mismatches
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US-10-039-785-53
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; OTHER INFORMATION: T1006F07 scFv
US-10-039-785-53
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                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 53
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LENGTH: 109
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Patent No. 626223
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CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL TITLE OF INVENTION: Receptors
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EARLIER FILING DATE: 1994-07-15
NUMBER OF SEQ ID NOS: 10
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                                                                                                                                                                NUMBER OF SEQ ID NOS:
                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
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                                         ORGANISM: Artificial sequence FEATURE:
                                                                                                     ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/341,237 FILING DATE: 2001-12-20
                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                FILING DATE: 2001-08-02
APPLICATION NUMBER: 60/294,981
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/323,807
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/327,364 FILING DATE: 2001-10-09
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Pred. No.
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26;
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                                                                                            US-09-025-769B-51
                                                                                                            RESULT 14
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                                           Sequence 51, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., 1
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Protein/(Poly)peptide libraries NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
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APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
                                 APPLICANT:
    APPLICANT:
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nes 5; Conserv
                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
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1251 Avenue of the Americas
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Ilag, Vic
                 Knappik,
Pack, Pet
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71.4%;
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Pred. No. 63;
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US-09-372-425A-4
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                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09372425A Patent No. 6475749
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APPLICANT: Sherie L. Mori
APPLICANT: Ramon Montano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
                                                                                                            ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                  STREET: 2000
CITY: Los Angeles
CTATE: CA
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ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 18-FEB-
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Improved Rh Antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 5; Conserv
APPLICATION NUMBER: US/09/372,425A FILING DATE: August 11, 1999 CLASSIFICATION: 435
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TOPOLOGY: linear
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                                                                 MEDIUM TYPE: Ploppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 98
SOPTWARE: MS Word
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VENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                USA
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(212)596-9090
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Pred. No.
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st, Suite 3800
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Oldenakmp, David J.
REGISTRATION NUMBER: 29,421
REGISTRATION NUMBER: 510015-223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 234 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: Light chain - AA
US-09-372-425A-4

Query Match
Best Local Similarity 71.4%; Pred. NO. 94;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;
Db 69 DNNQRPS 75

Search completed: January 12, 2004, 07:04:02
Job time: 6.79688 secs
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Result
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A46271	B84931	A40526	IJHULM	G87767	S60464	T02398	JQ1894	A84787	T10374	VCNV87	B96560	T52115	T16041	S63360	T15069
integrin beta-7 ch	DNA topoisomerase	integrin beta-7 ch	leukocyte adhesion	protein mes-3 [imp	mes-3 protein - Ca	hypothetical prote	hypothetical 74.1K	hypothetical prote	p87 capsid protein	p87 capsid protein	hypothetical prote	myrosinase-binding	hypothetical prote	hypothetical prote	hypothetical prote

ALIGNMENTS

internal in like protein (LPXTG motif) [imported] - Listeria innocua (strain Clip11262) (;Species: Listeria innocua (;Species: Listeria innocua (;Species: Listeria innocua (;Pate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001 (;Paccession: AC1469 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, I D.; Jones, L.M.; Karst, U. Science 294, 849-852, 2001 R.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; I A;Authors: Kreft, J.; Kuhn, M., Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; I Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-680 <GES> A;Cross-references: EMBL:Y11483; NID:e1023101; PIDN:CAA72271.1; PID:e304150 A;Experimental source: cv. Global; idolate a4; young seedlings probable myrosinase-binding protein - rape N;Alternate names; jasmonate inducible protein C;Species: Brassica napus (rape) C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000 C;Accession: T08080 R;Geshi, N.; Brandt, A. Planta 204, 295-304, 1998 A;Reference number: Z16340; MUID:98192006; PMID:9530873 A;Accession: T08080 S A; Molecule type: DIA A; Residues: 1-505 <GLA> A; Residues: 1-505 <GLA> A; Cross-references: GB: AL592022; PIDN: CAC95523.1; PID: g16412719; GSPDB: GN00178 A; Experimental source: strain Clip11262 C; Genetics: A; Gene: lin0290 밁 A; Status: preliminary A;Note: T08080 Best Local Matches Query Match N jasmonate inducible 319 TYDNSNVV 326 1 SYDSSNVV 8 Similarity Conservative 84.6%; 75.0%; Score 33; Pred. No. Mismatches 38; DB 2 0, Length 505; G.; Madueno, E.; Maitournam, A.; Mauez-Boland, J.A.; Voss, H.; Wehland, Indels 0, Brassica napus L. Gaps 0, ; Bloecker Fsihi, H seed Ma

T23806 T17613

probable receptor chitin synthase (E replication protei probable membrane

hypothetical prote hypothetical prote hypothetical prote

Query Match

84.6%;

Score 33;

DB 2;

Length 680

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Ryfiheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alone Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, R. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Lil, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: F96559
                                                                                                                                                                                                                                                                                A;Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAI A;Experimental source: serotype O2, strain NCTC 11168
A;Note: a translation exception was noted by the authors
A;Note: in Genbank entry AL139078, realease 117.0, PIDN:CAB73932.1, C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The genome sequence of the food-borne pathogen A;Reference number: A81250; MUID:20150912; PMID:10688204 A;Accession: C81298
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R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, C.W.; Ouall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
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A;Residues: 1-730 <STO>
A;Cross-references: GB:
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C;Species: Arabidopsis thaliana (mouse-ear
C;Date: 02-Mar-2001 #sequence_revision 02-
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                                                                                                 ;Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein; 57,60,64,92/Binding site: 4Fe-4S cluster (Cys) (covalen; 94,182/Active site: Lys, His #status predicted; 181/Binding site: molybdopterin guanine dinucleotide (C;181/Modified site: selenocysteine #status predicted
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C.Species: Rattus sp. (rat)
C.Japecies: Rattus sp. (rat)
C.Japecies: Rattus sp. (rat)
C.Japecies: A60163
C.Jate: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 13-Sep-1998
C.Jate: 12-Feb-1993 #sequence not 12-Feb-1993 #text_change 13-Sep-1998
C.Jacession: A60163; #60163; #1900
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A.Jitle: Analysis of rodent platelet glycoprotein IIb: evidence for evolutionari
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A;Title: Plexin A is a neuronal semaphorin receptor that cont A;Reference number: Z17621; MUID:99091049; PMID:9875845
A;Accession: T13937
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  Ig lambda chain V-VI region (Nig-48) -
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1980 #sequence_revision
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C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-
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A; Cross-references:
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A; Residues: 1-1945 <WIN>
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protein F47F6.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: E88040
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Gerischer, U.; Duerre, P.
J. Bacteriol. 172, 6907-6918, 1990
A;Title: Cloning, sequencing, and molecular analysis of A;Reference number: A37837; MUID:91072241; PMID:2254264
A;Accession: B37837
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R;Takahashi, N.; Takayasu, T.; Isobe, T.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 86, 1523-1535, 1979
A;Title: Comparative study on the structure of the light chains of human immunoglobulins A;Reference number: A01991; MUID:80094390; PMID:118171
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C;Species: Clostridium acetobutylicum
C;Species: C-2-dan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999
C;Accession: B37837
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-112 <TAK>
A;Note: this is the first sequenced V region C;Comment: This is a Bence Jones protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M55392; GB:M34078; NID:g144708; PIDN:AAA63759.1; PID:g144709 C;Superfamily: alpha-amylase, subtilis type; alpha-amylase core homology C;Keywords: glycosidase; hydrolase
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A; Residues: 1-469 < GER>
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A;Map position: 22q11.2-22q11.2
                                                                                                                                                                                                                                                                                                                                                                      E88040
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Best Local
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                                                Status: preliminary
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type: DNA
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85.7%;
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Pred. No. 12;
1; Mismatches
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Pred. No.
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12;
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유 성

83

SYDSSNV 7

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hypothetical protein F11C1.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T20762 R;Palmer, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: F47F6.3
A;Map position:
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S58356
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T20762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Meyer, C.; Bierbaum, G.; Heidrich, C.; Reis, M.; Sueling, J.; Iglesias-Wind, M.I. Eur. J. Biochem. 232, 478-489, 1995
A;Title: Nucleotide sequence of the lantibiotic Pep5 biosynthetic gene cluster and A;Reference number: 866651; MUID:96035882; PMID:7556197
A;Accession: S66651
                                                                                                                          A;Residues: 1-130 <WIL>
A;Cross-references: EMBL:Z54270; PIDN:CAA91026.1; GSPDB:GN00028; CESP:F11C1.2
A;Experimental source: clone F11C1
                                                                                                                                                                                                        submitted to the EMBL Data Library, A;Reference number: Z19321
A;Accession: T20762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Staphylococcus epidermidis
C;Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 02-Feb-2001
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                                                                                A;Map
                                                                                             A; Gene: CESP:F11C1.2
                                                                                                                                                                            A; Molecule type: DNA
                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: pepT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:Z49865; NID:g945014; PIDN:CAA90021.1; PID:g945015
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Query Match
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Best Local S
Matches 6
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75.0%;
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75.0%;
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Pred. No. 71;
1; Mismatches
Score 31; DB
Pred. No. 24;
1; Mismatches
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24;
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A; Molecule type: mRNA
A; Residues: 1.245 <SHI>
A; Residues: 1.245 <SHI>
A; Residues: 1.245 <SHI>
A; Residues: 1.245 <SHI>
A; Cross-references: GB:J03606; NID:g205331; PIDN:AAA41582.1; PID:g205332
A; Cross-references: GB:J03606; NID:g205331; PIDN:AAA41582.1; PID:g205332
A; Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
Biochemistry 26, 4605-4610, 1987
A; Title: A cDNA presumptively coding for the alpha subunit of the receptor w
A; Fitle: A cDNA presumptively coding for the alpha subunit of the receptor w
A; Reference number: A27116; MUID:88024987; PMID:2959318
A; Accession: A27116
A; Molecule type: mRNA
A; Residues: 1, 'G',3-236,'N',238-244,'RLKPNS' <KIN>
A; Tepler: 1, Shimizu, A.; Leder, P
J. Biol. Chem. 264, 5912-5915, 1989
A; Title: The gene for the rat mast cell high affinity IgE receptor alpha cha
A; Reference number: I55304; MUID:89174653; PMID:2522441
A; Reference number: I55304; MUID:89174653; PMID:2522441
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(A) Alternate names: Fc-epsilon-R alpha chain precursor

(A) Species: Rattus norvegicus (Norway rat)

(C) Pate: 18-Oct-1989 #sequence revision 18-Oct-1989 #text_change 21-Jan-2000

(C) Accession: C31377; A31327; A30154; A77116; I55304

(R) Liu, F.T.; Albrandt, K.; Robertson, M.W.

(Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988

(A) Fitle: cDNA heterogeneity suggests structural variants related to the high

(A) A; Reference number: A94203; MUID:88289772; PMID:2969594

(A) A; Molecula type: mRNA

(A) A; Molecula type: mRNA

(A) A; MOLECULA (A) A; MOLECULA (B) A; MOLECULA 
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A;Residues: 21-245 <LI3>
A;Cross-references: GB.M21622; NID:g204109; PIDN:AAA41146.1; PID:g204110; GB:J03811
A;Experimental source: basophilic leukemia cell line
R;Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder,
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A;Title: Human and rat mast cell high-affinity immunoglobulin E receptors: character
A;Reference number: A94191; MUID:88158102; PMID:2964640
A;Accession: A30154
                                                                                                                                                                          R; Lin, X.; Kaul, S.; M.; Koo, H.; Moffat,
                                                                                                                                                                                                                                                             hypothetical protein At2g36540 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: G84781
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A; Residues: 1-16 < RES>
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A;Experimental source: basophilic leukemia cell line,
A;Accession: A31327
                                                        A;Title:
                                                                                           Nature 402, 761-768,
                                                                                                                                   euss, D.; Nierman, W.C.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;1-23/Domain: signal sequence #status predicted <SIG>
;24-245/Product: IgE receptor alpha chain #status predicted <MAT>
;42-93/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cross-references: GB:M25334; NID:g341335; PIDN:AAA74562.1; PID:g556391; Superfamily: Fc gamma receptor III; immunoglobulin homology; Keywords: immunoglobulin receptor; transmembrane protein
                 Reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 
nes 5; Conserv
        Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana nce number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYDSNNI 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYDSSNV
                                                                                                                              S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, fat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Talln, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                       1999
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71.4%;
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Pred. No. 47;
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                                                                                                                                   J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
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T15520
A;Molecule type: protein
A;Residues: 20-25,'x',27-28,'x',30-36,'x',38-39 <SHI>
A;Residues: 20-25,'x',27-28,'x',30-36,'x',38-39 <SHI>
C;Comment: This protein has essential roles in the regulation and coordination of insulily a role during myoblast proliferation and differentiation, and is important in the glays a role during myoblast proliferation and differentiation, and is important in the gC;Superfamily: insulin-like growth factor binding protein 1; thyroglobulin type I repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
JC4584
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R;Bentley, D
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A;Gene: At2g36540
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A;Cross-references: GB:U41340; NID:g1173906; PIDN:AAA87859.1; PID:g1173907 A;Experimental source: skeletal muscle R;Shinasaki, S.; Gao, L.; Shimonaka, M.; Ling, N. Mol. Endocrinol. 5, 938-948, 1991
A;Title: Isolation and molecular cloning of insulin-like growth factor-bin A;Reference number: A23734; MUID:92049376; PMID:1719383
A;Accession: G23734
                                                                                                                                                                                                                                 insulin-like growth factor binding protein-5 precursor - pig (;Species: Sus scrofa domestica (domestic pig) (;C;Date: 10-Apr-1996 #sequence_revision 24-May-1996 #text_change 19-Jul-2002 C;Accession: JC4584; G23734 R;White, M.B.; Diao, R.; Hathaway, M.R.; Mickelson, J.; Dayton, W.R. Biochem. Biophys. Res. Commun. 218, 248-253, 1996 A;Title: Molecular cloning and sequence analysis of the porcine insulin-like A;Reference number: JC4584; MUID:96136309; PMID:8573141
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R;Bentley, D.

submitted to the EMBL Data Library, April 1996

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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T15520
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-249 <STO>
A;Cross-references: GB:AE002093; NID:g4581152; PIDN:AAD24636.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U56965; NID:g1945492; PID:g1293841; PIDN:AAB52662.1; GSPDB:GN00
A;Experimental source: strain Bristol N2; clone C15H9
C;Genetics:
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A; Residues: 1-261 <BEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein C15H9.2 - Caenorhabditis elegans C; Species: Caenorhabditis elegans
                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-271 <WHI>
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Pred.
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Pred. No.
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Page 5
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C;Keywords: differentiation; skeletal muscle
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: insulin-like growth factor binding protein-5 #status experimental <MAT
F;20-271/Product: insulin-like growth factor binding protein-5 #status experimental <MAT
F;191-262/Domain: thyroglobulin type I repeat homology <THY1>

Query Match
Best Local Similarity 85.7%; Score 31; DB 2; Length 271;
Best Local Similarity 85.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYDSSNV 7
Db 264 SFDSSNV 270

Search completed: January 12, 2004, 07:03:10

Job time: 10:25 secs

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Result
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39
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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VAAL MOUSE
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COAB BPIF1
AMY CLOAB
FCEI RAT
IBPS PIG
SER3 DROME
FOLE CANAL
PRZN RENSA
CHS2 YEASTI
REGA CLOSA
YN8H YEASTI
VP87 HUMAN
ITB7 HUMAN
GYRB BUCAI
GYBT BUCAI
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O80297 bacteriopha
P23671 clostridium
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P1665
P165107
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28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
J. Bacteriol. [4]
                       MEDLINE=21359325; PubMed=11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Tatusov R.L., Sabathe F., Doucette-Stamm L., Souca Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative Danalysis of the sbacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
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STRAINATCC 824 / DSM 792 / VKM B-1787;

STRAINATCC 824 / DSM 792 / VKM B-1787;

Sabathe F., Cornillot E., Croux C., Soucaille P.;

Sabathe F., Cornillot E., Croux C., Soucaille P.;

Molecular characterization of amyP, a pSOL1 located major alpha-amylase of Clostridium acetobutylicum ATC as a reporter system for strain degeneration.";

submitted (JUN-1999) to the EMBL/GenBank/DDBJ databas
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STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
Schaffer S., Duerre P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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Pred. No. 21;
1; Mismatches
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; 9AD651968C715AB2 CRC64;
                                                                                                                                                                                                          B-1787;
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ATCC824, and its
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01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
High affinity immunoglobulin epsilon receptor alpha-subunit pr
(FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon.RI-alpha)
FCERIA OR FCEIA.
                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                       FCE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00128; alpha-amylase; 1. Pfam; PF02806; alpha-amylase_C; 1. Pfam; PF03423; CBM_25; 1.
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STRAIN=ATCC 824 / DSM 792 / VKM B
MEDLINE=91072241; PubMed=2254264;
Gerischer U., Duerre P.;
                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00632; Aamy_C;
Hydrolase; Glycosidase;
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InterPro; IPR006047; Alpha_amyl_cat.
InterPro; IPR005085; CBM_25.
InterPro; IPR006046; GlyCo_hydro_13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
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J. Bacteriol. 172:6907-6918(1990)
  MEDLINE=88024987; PubMed=2959318
            SEQUENCE FROM N.A
                                NCBI_TaxID=10116;
                                                                      Rattus norvegicus (Rat).
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                                              Craniata; Vert
Sciurognathi;
                                                                                                                                                                                                                                                                                                                               10E146F40252F6D0 CRC64;
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                                               Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
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Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643 (1988).

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EMBL; J03606; AAA41582.1; -.
EMBL; M21622; AAA41146.1; -.
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                                                                                                                                                                                                                                                                                                                                            Pfam; PF00047; ig; SMART; SM00409; IG;
                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
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MEDLINE=88158102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A cDNA presumptively coding for the alpha with high affinity for immunoglobulin E."; Biochemistry 26:4605-4610(1987).
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                                                                                                                                                                                                                                                                             SIGNAL
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Liu F.-T., Albrandt K., Robertson M.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shimizu A.,
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r I., Benfey P.N.,
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in; Receptor;
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IG-LIKE 1.

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                                                  N-LINKED
                                                                                                                                                                                                                                          HIGH AFFINITY IMMUNOGLOBULIN RECEPTOR ALPHA-SUBUNIT
                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Signal;
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RESULT 6
IBP5_PIG
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Best Local Similarity
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Best Local
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01-NOV-1997
01-NOV-1997
28-FEB-2003
                                                                               DOMAIN
SEQUENCE
                                                                                                                         SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                         InterPro; IPH000867; Insl gro fac pr.
InterPro; IPR000716; Thyroglobulin_1.
pfam; pF00219; IGFBB; 1.
pfam; pF00086; thyroglobulin_1; 1.
SMART; SM00121; IB; 1.
SMART; SM00211; TY; 1.
                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 IGFBP domain.
-!- SIMILARITY: Contains 1 thyroglobulin type-I domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                White M.E., Diao R., Hathaway M.R., Mickelson J., Dayton W.R.; "Molecular cloning and sequence analysis of the porcine insulin-like growth factor binding protein-5 complementary deoxyribonucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Insulin-like growth factor binding protein 5
(IBP-5) (IGF-binding protein 5).
                                                                                                                                                           PROSITE; PS00222; IGF BINDING; 1.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
                                                                                                                                                                                                                                                                                                      EMBL; U41340; AAA87859.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96136309;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       PIR; JC4584; JC4584.
                                                                                                                                                                                                                                                                            HSSP; P24593; 1BOE
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 SYDSSNV 7
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271
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                           Conservative
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30323 MW;
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                                      79.5%;
85.7%;
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71.4%;
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Pred. No. 17;
                                       Score 31; DB
Pred. No. 19;
                                                                                                           INSULIN-LIKE PROTEIN 5.
                                                                                              THYROGLOBULIN TYPE
                                                                                                                                      POTENTIAL
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                                                                                 95C254E95DC4ED8D
                         Mismatches
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Sus.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., RA Adams M.D., Celniker S.E., Holt R.A., How, Hoskins R.A., Galle R.F., RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Levis S.E., Richards S., Ashburner M., Henderson S.N., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., RA Sutton G.G., Rogers Y.-H.C., Blazel R.G., Champe M., Ffeiffer B.D., RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Maril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D., Basul A., Baxendale J., Bayrakacarglu L., Beasley E.M., Ra Beson K.Y., Banos P.V., Berman B.P., Bhandari D., Bolshakov S., Ra Grey J.M., Cawley S., Dahke C., Davenport L.B., Davies P., Ra Gerbahos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Gelbahos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Hollin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Ra Glodek A., Gong F., Gorrell J.H., Gu Z., Ghan P., Harris M., Harvis N.I., Harvey D., Heiman T.J., Hermandez J.R., Houck J., A Harris N.I., Harvey D., Heiman T.J., Hermandez J.R., Houck J., A Hasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Li X., Mattei B., McIntosh T.C., McLeod M., McShue B.C., Staplen G.H., Ke Z., Kennison J.A., Ketchm K.A., Akimel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Li X., Mattyp D., Lai Z., Liang Y., Lin X., Li X., Mattyp G., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Ra Nelson D.R., Nelson K.A., Saunders R.D. C., Scheeler F., Shen H., Shue B.C., Stone F.N., Nang A.H., Wang X., Shen M., Scheeler F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Thang Y., Zhong Y., Zhon W., Smith H.O., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SER3 DROME
P17207; Q9VA
01-AUG-1990
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
Serine protease 3 precursor (EC 3.4.21.-).
SER99DC OR SER3 OR CG17951.
                                                                                                                               "Levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hrazapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DROME
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NCBI_TaxID=7227;
                                                                                           cyclic AMP.
Mol. Cell.
                                                                                                                                                                   MEDLINE=89219063;
Yun Y., Davis R.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
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CORTINUED TO INCREASE IN PUPPAE BUT REAPPEARED IN THE ADULT.
THEY ARE NOT PRESENT IN PUPPAE BUT REAPPEARED IN THE ADULT.
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264 SFDSSNV 270
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Drosophila
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PubMed=2469005;
                                                                                                                               family of putative melanogaster dunce
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-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

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15-SEP-2003
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CONFLICT
SEQUENCE
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SMART; SM00020; Tryp SPC; 1.
PROSITE; PS50240; TRYPSIN DOM;
PROSITE; PS00134; TRYPSIN HIS;
PROSITE; PS00135; TRYPSIN SER;
                                                                                SEQUENCE FROM N.A.
Subramanian M., Li C., DeSouza L.,
Suequencing of a Candida albicans
encodes the complete open reading
                                                                                                                                              Candida albicans (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                        FOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for cor
                                                                                                                                                                                                                                  Q9Y893;
15-SEP-2003
                                                                                                                                                                                                                                                                   CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00089; trypsin; I.
PRINTS; PR00722; CHYMOTRYPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M24380; AAB025
PIR; PS0049; PS0049.
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                                                             Submitted (JUN-1999)
                                                                        synthetase.";
                                                                                                                                     NCBI_TaxID=5476;
                                                                                                                                                                                       synthetase)
                                                                                                                                                                                                 Folylpolyglutamate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001314; Chymotrypsin.
InterPro; IPR001254; Ser protease_Try.
Pfam; PF00089; trypsin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgn0003358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
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similarity).

Similarity).

CATALYTIC ACTIVITY: ATP + {tetrahydrofoly1-[Glu]}(N) + L-glutamate = ADP + phosphate + {tetrahydrofoly1-[Glu]}(N+1).

SIMILARITY: Belongs to the foly1polyglutamate synthase family.
                                                  FUNCTION: Conversion
                                                                                                                                                                                                                                                         CANAL
                                                                                                                                                                                                                                                                                                             171 YDGSNVV 177
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272
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17
POTENTIAL.
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BY SIMILARITY
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85.7%;
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                                                                                                      DeSouza L.,
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                                                 EMBL/GenBank/DDBJ databas folates to polyglutamate
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                                                                                                                                                                                                                                                                                                                                                                 Score 31;
Pred. No.
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                                                                                                                                               Saccharomycotina; Saccharomycetes; Saccharomycetales; Candida.
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A61E9DE3AFCA93AF
                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                , Bognar A.L.;
genomic library plasmid which
frame of folylpolyglutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RELAY SYSTEM
RELAY SYSTEM
RELAY SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zymogen;
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                                               databases.
utamate derivatives
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P55111;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RENSA
                                                                                                                                                           between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an analysis of the statement is not removed.
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grayson T.H.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ZINC METALLOPROTEASE WITH HEMOLYTIC PROPERTIES.
-!- PUNCTION: ACTIVITY IS OBSERVED FROM 6 TO 37 DEGREES CELS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95400487; PubMed=7545509;
Grayson T.H., Evenden A.J., Glipin M.L., Martin K
"A gene from Renibacterium salmoninarum encoding a
shows homology to bacterial zinc-metalloproteases
Microbiology 141:1331-1341(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01011; FOLYLPOLYGLU_SYNT_1; FALS
PROSITE; PS01012; FOLYLPOLYGLU_SYNT_2; 1.
Ligase; One-carbon metabolism; ATP-Dinding
NP_BIND 78 84 ATP (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                       entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                          -I- FUNCTION: ZINC METALLOPROTEASE WITH HEMOLYTIC PROPERTIES.

HEMOLYTIC ACTIVITY IS OBSERVED FROM 6 TO 37 DEGREES CELSIU MAMMALIAN ERVIFROCYTES.

-I- COFACTOR: Binds 1 zinc ion and 4 calcium ions per subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=MT444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Zinc metalloproteinase precursor (EC 3.4.24.-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001645; Ppolygl synthtse
TIGRFAMs; TIGR01499; folC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Actinobacteria; Actinobacteridae; Ao
Micrococcineae; Micrococcaceae; Renibacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Renibacterium salmoninarum.
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SUBCELLULAR LOCATION: NOT SECRETED,
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                                                                                                           email to license@isb-sib.ch).
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X76499;

1HYT CAA54032.

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R MEROPS; M04.UPW; ...

R InterPro; IPR001570; Peptidase M; ...

JR Pfam; PF01447; Peptidase M4; 1.

DR Pfam; PF01447; Peptidase M4; C; 1.

Pfam; PF02868; Peptidase M4 C; 1.

DR PRINTS; PR00730; THERMOLYSIN.

DR PRINTS; PR00742; ZINC_ PROTEASE; 1.

ET PROPER 1 28 POTENTIAL.

FT ROPER 29 ? POTENTIAL.

FT ROPER 29 ? POTENTIAL.

FT ROPER 29 ? POTENTIAL.

FT ROPER 362 ZINC (CATALYTIC) (BY SIMILARITY).

FT ACT_SITE 363 363 EXINC (CATALYTIC) (BY SIMILARITY).

FT METAL 366 366 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 386 386 ZINC (CATALYTIC) (BY SIMILARITY).
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CHS2_YEAST
ID CHS2_Y
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CHS2 OR YBR038W OR YBR0407.
                                                                                                                                                                                                                                                           Andre B.,
Vissers S.
This
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=90143137; Silverman S.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
MCBI_TaxID=4932;
                                                                                                                                          Implication sites.";
                                                                                                                                                                  MEDLINE=95293998; PubMed=7775457;
Nagahashi S., Sudoh M., Ono N., Sawada R., Y
Mio T., Takagi M., Arisawa M., Yamada-Okabe
"Characterization of chitin synthase 2 of Sa
                                                                                                                                                                                                                                                                                                                           "Similar and different do cerevisiae: two isozymes Yeast 5:459-467(1989).
                                                                                           -
                                                                                                                               J. Biol.
                                                                                                                                                                                                                                                                                      STRAIN=S288c;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P14180;
                                                                                                                                                                                                                        MUTAGENESIS
                      BIOI. Chem. 270:13961-13967(1995).

BIOI. Chem. 270:13961-13967(1995).

FUNCTION: ESSENTIAL FOR SEPTUM FORWATION AND CELL DIVISION FUNCTION: REQUIRED FOR MAINTAINING NORMAL CELL MORPHOLOGY.

IS REQUIRED FOR MAINTAINING NORMAL CELL MORPHOLOGY.

CATALYTIC ACTIVITY: UDP-N-accetyl-D-glucosamine + {(1,4)-(N-accetyl-beta-D-glucosaminyl)}(N) = UDP + {(1,4)-(N-accetyl-beta-D-glucosaminyl)}(N+1).

ENZYME REGULATION: REQUIRES PROTEOLYTIC ACTIVATION.

SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO THE CHITIN SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YEAST
 SWISS-PROT
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Last annotation update)
2.4.1.16) (Chitin-UDP a
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C:
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Pred. No.
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distinct functions.";
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 produced through a collaboration
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5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)

(POTENTIAL).

(POTENTIAL)

PXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).

ACTIVITY.

CYTOPLASMIC (POTENTIAL).

8 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

N-A: 30% DECREASE OF ACTIVITY.

N-A: 30% DECREASE OF ACTIVITY.

D-A: 10% DECREASE OF ACTIVITY.

D-A: 5% DECREASE OF ACTIVITY.

D-A: 5% DECREASE OF ACTIVITY.

N-A: 80% DECREASE OF ACTIVITY.

N-A: 80% DECREASE OF ACTIVITY.

N-A: 90% DECREASE OF ACTIVITY.

N-A: 60% DECREASE OF ACTIVITY.

N-A: 90% DECREASE OF ACTIVITY.

N-A: 100S OF ACTIVITY.

LOSS OF ACTIVITY.

60% DECREASE OF ACTIVITY.

NO CHANGE IN ACTIVITY.

85% DECREASE OF ACTIVITY.

95% DECREASE OF ACTIVITY.

95% DECREASE OF ACTIVITY.

ACTIVITY

A: 10% DECREASE OF ACTIVITY.
A: 54% DECREASE OF ACTIVITY.
A: LOSS OF ACTIVITY.
B: LOSS OF ACTIVITY.
B: LOSS OF ACTIVITY.
A: 70% DECREASE OF ACTIVITY.
A: 70% DECREASE OF ACTIVITY.
A: 80% DECREASE OF ACTIVITY.
A: 95% DECREASE OF ACTIVITY.
A: 95% DECREASE OF ACTIVITY.
A: 90% DECREASE OF ACTIVITY.
A: 90% DECREASE OF ACTIVITY.
A: 60% DECREASE OF ACTIVITY.
A: 90% DECREASE OF ACTIVITY.

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EMBL; M23865; AAA34493.1; -.
EMBL; Z35907; CAA84980.1; -.
PIR; S45167; S45167.
SGD; S0000242; CHS2.
GO; GO:0000142; C:contractile ring (sensu Sacc GO; GO:000140; F:chitin synthase activity; ID GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016288; P:cytokinesis; IMP.
GO; GO:0016280; P:response to osmotic stress; InterPro; IPR004934; Chitin synth.
InterPro; IPR001173; Glyco trans_2.
Pfam; PF01644; Chitin synth; 1.
ProDom; PD002998; Chitin synth; 1. Transferase; Glycosyltransferase; Multigene family. EXTRACELLULAR (POTENTIAL).

1 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

3 (POTENTIAL). Transmembrane; Cell wall; Saccharomyces); IMP.

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RESULT 11
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P70873;
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Submitted (NOV-1996) to the EMBL/GENBAN/CIDBJ databases.
-i- FUNCTION: PRODUCES CYCLOISOMAL/GOOLIGOSACCHARIDE FROM DEXTRAN.
-i- SIMILARITY: BELONGS TO FAMILY 66 OF GLYCOSYL HYDROLASES.
                                                                               SEQUENCE
                                                                                                                  InterPro; IPR005084; CBM_6.
Pfam; PF03422; CBM_6; 2.
Transferase; Glycosyltransferase; Signal.
                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last amotation update)
(Cycloisomaltooligosaccharide glucanotransferase
                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=1397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                    EMBL; D88360; BAA13595.1; -.
                                                                                                                                                                                  entities requires a license
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Bacteria; Firmicutes;
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SYDSSN 526
                                                                              964 AA;
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85.7%;
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                                                                              MW;
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                                      Score 31; DB; Pred. No. 80; 0; Mismatches
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R->K:
W->A:
                                                                             POTENTIĀL.
CYCLOISOMALTOOLIGOSACCHARIDE
GLUCANOTRANSFERASE.
W; 8849CDC5E2DE9A68 CRC64;
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R->K: 57% DECREASE OF ACTIVITY
RR->KK: LOSS OF ACTIVITY.
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->K: LOSS OF ACTIVITY.
->A: LOSS OF ACTIVITY.
->Y: LOSS OF ACTIVITY.
->Y: LOSS OF ACTIVITY.
->A: 95% DECREASE OF ACTIVITY.
4D44A287C0B65B5B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     964
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                                               .
80;
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RESULT 12

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YN8H_YEAST
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Matches 5
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Q45831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Davison S.P., Santangelo J.D., Reid S.J., Wo Pavison S.P., Santangelo J.D., Reid S.J., Wo Pavison In Activation regulator gene production in Bacillus subtilis.", Microbiology 141:989-996 (1995).
-!- FUNCTION: INVOLVED IN THE REGULATION OF
                                                                                                        YN8H YEAST STANDARD; PRT; 429 AA. P53729; (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update) Hypothetical 48.1 kDa protein in SEC12-SSK2 in YNR029C OR N3260.
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001761; PerTplaBP/Lac1.
pfam; pF00356; lac1; 1.
pfam; pF00356; lac1; 1.
pfam; pF00352; Perripla BP_like; 1.
prINTS; pR0036; HTHLACI.
pRINTS; pR00354; HTH LACI; 1.
pROSITE; pS00356; HTH LACI; 1.
pROSITE; pS00356; HTH LACI; 1.
prosite; pS00356; HTH LACI FAMILY; 1.
Transcription regulation; DNA-binding.
Transcription regulation; DNA-binding.
DNA_BIND
5 24 H-T-H MOTIF (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLOSA
Submitted (MAY-1996)
                                                                 Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L14685; AAA23275.1; -. HSSP; P15039; 1PRU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=P262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clostridium saccharobutylicum.
Racteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGA OR REPA.
           SEQUENCE FROM N.A. Pohl T.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE LACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95291448; PubMed=7539689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=169679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulatory protein regA.
                                                   NCBI_TaxID=4932;
                                                                                            Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel.
15-JUL-1998 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nterPro; IPR000843; HTH_LacI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAUTION: Was originally thought to originate C.acetobutylicum.
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332 AA; 37260 MW;
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40,
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to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                               Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                         27CBE52FF9BEB007 CRC64;
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                                                                    Saccharomyces
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                                                                                                                      intergenic region
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RESULT 14
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RX MEDININE=21016719; pubMed=11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RH Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

RA Hinter J.J., Jee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee A., Lucos J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9SAVO;
16-OCT-2001
16-OCT-2001
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheog
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003495; CobW.

Pfam; PP02492; cobW; ATP-binding.

Hypothetical protein; ATP-binding.

NP_BIND 78 85 ATP (
                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
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MEDLINE=90232722; PubMed=2184573;
Mueller R., Pearson M.N., Russell R.L.Q., Rohrmann G.K.;
Mueller R., Pearson M.N., Russell R.L.Q., Rohrmann G.K.;
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""" ransid-associated protein of the multicapsid nuclear position, sequence
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P87.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Orgyia pseudotsugata multicapsid polyhedrosis virus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
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Virology 229:381-399(1997).
-!- SUBCELLULAR LOCATION: CAPSID-ASSOCIATED.
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SUMMARIES

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SEQUENCE
                                                                                                                                                                      "Two jasmonate inducible proteins from Brassica napus seedlings homologous to myrosinase binding proteins and jacalin."; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. EMBL; Y11483; CAA77271.1; -. HSSP; P18670; IJAC. HSSP; P18670; IJAC. InterPro; IPR001229; Jacalin lectin.
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; AF469056; AAN32885.1; -.
SEQUENCE 600 AA; 66232 MW; 67069EF6C12445A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Brassica.
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Tylenchoidea; Heteroderidae; Heteroderinae;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                          Geshi N., Brandt A.;
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                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape)
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Q9ZU23;
01-MAY-1999
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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"Arabidopsis thaliana chromosome 1 BAC F5F19 sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
              MEDLINE-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen Campylobacter jeju
reveals hypervariable sequences.";
Nature 403:65-668(2000).
EMBL; AL139078; CAB73932.1; -.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bacteria; Proteobacteria;
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Pfam; PF01419; Jacalin; 3.
PROSTTE; PS00225; CRYSTALLIN BETAGAMMA;
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Wan K.H., Doyle C., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotties P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotties P.,
RA Gebon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Jevitski A.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Sigletin R., Scholar B., Weinstock G.M., Weissenball J..
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                        Wang Z.Y., Wassarman D.A., Weins Williams S.M., WoodageT, Worley
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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PP04879; Molybdop P6484; 1.
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AMS; TIGR01409; TAT signal seq; 1.
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"Sequencing of Drosophila melanogaster genome.";
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[2]
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                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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                  MEDLINE=99091049, PubMed=9975845;
Winberg M.L., Noordermeer J.N., Tamagnone L.,
Spriggs M.K., Tessier-Lavigne M., Goodman C.S.
"Plexin A is a neuronal semaphorin receptor th
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PLEXA OR CG11081.
                                                                                                                                                                                                                                                                                                                                           01-MAY-1999
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R.A., Myers E.W., Rubin G.M.,
genome sequence of Drosophila
ce 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE003846; AAN06564.1;
NCE 1505 AA; 170234
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                                                                                                                      FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AANSSUAS
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                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                 N.A.
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MW;
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                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 5;
Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Venter
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                       that controls axon
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J databases
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                                                                     Comoglio P.M.,
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Glabart W.M., Glasser K.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Mulson K.A., Nicon K., Nusskern D.R., Pacleb J.M.,
RA Mount S.M., Nelson K.A., Nicon K., Nusskern D.R., Pacleb J.M.,
RA Rainert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Rainert M., Skupski M.P., Smith T.,
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Best Local
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InterPro; IPRO03659; Ple
InterPro; IPRO02165; Ple
InterPro; IPRO02165; Sen
InterPro; IPRO00215; Sen
InterPro; IPRO00215; Ser
Pfam; PPO1403; Sema; 1.
Pfam; PPO1403; Sema; 1.
Pfam; PPO1833; TIG; 3.
SMART; SMO0429; IPT; 3.
SMART; SMO0429; IPT; 3.
SMART; SMO0429; SER; 3.
SMART; SMO0630; Sema; 1.
PROSITE; PSO0384; SERPIN
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InterPro; IPR002909; IPT TIG.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
InterPro; IPR001627; Sema.
InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9V491;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=7227;
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mes 5; Conserv
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SYESSNII 1273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218278 MW;
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13,
23,
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Fleischmann W.,
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RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Wyers E.W., Rubin G.M., Yenter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RI Science 287:2185-2195(2000).

DR Edwig A.BO03346; AAR59394.1; -.

DR InterPro; IPR002165; Plexin-like.

DR InterPro; IPR002165; Plexin-like.

DR InterPro; IPR002167; Sema.

DR InterPro; IPR002167; Sema.

DR InterPro; IPR000215; Sema.

DR Ffam; PF01437; PSI; 3.

DR Pfam; PF01433; Sema; 1.

DR Pfam; PF01833; TIG; 3.

DR Pfam; PF01833; TIG; 3.
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                           Query Match
Best Local S
Matches 6
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Best Local S
Matches 5
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SMART; SM00423; PSI; 3.
SMART; SM00630; Sema; 1.
PROSITE; PS00284; SERPIN
SEQUENCE 1945 AA; 218
                                                                                                                                                                                                                                                                                                                                                                                                                       Q99383;
Q99383;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                  MEDLINE=21440425; PubMed=11556712;
Gambley C.F., Thomas J.E.;
"Molecular characterisation of Banana mild mosaic virus,
                                                                                                                                                                                                      Gambley C.F., Thomas J.E.;
Submitted (OCT-2000) to the
                                                                                  SEQUENCE
                                                                                                                       Pfam; PF00286; virus_P-coat; 1.
                                                                                                                                                                                            ---
                                                                                                                                                                                                                                                         filamentous virus in Musa spp.";
Arch. Virol. 146:1369-1379(2001).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses,
                                                                                                                                                                                                                                                                                                                                                                                Banana mild mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=148879
                                                                                                           PRINTS; PR00232; POTXCARLCOAT.
                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE POTEXVIRUSES EMBL; AF314662; AAK28493.1; --
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UN-2001 (TrEMBLrel. 17, La
CT-2002 (TrEMBLrel. 22, La
protein (Capsid protein).
                                                                                                                                                                              (BY SIMILARITY)
  2 YDSSNVV
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                             Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 62.
                                                                                  238 AA;
                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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A; 218356 MW;
                                                                                26825 MW;
                                         82.1%;
85.7%;
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Last sequence update)
Last annotation update)
                              1;
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S WITH THE RNA TO FORM INFECTIOUS PARTICLES
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Pred. No.
                                           Score
Pred.
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                              Mismatches
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4.6e+02;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
A Ballew R.M., Baybayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
A Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
A Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local :
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01-MAY-2000
01-MAY-2000
01-MAR-2003
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Goetz R., Huth W., Lesemann D.E., Maiss E.;
Goetz R., Huth W., Lesemann D.E., Maiss E.;
Molecular and serological relationships of Spartina mottle virus
(SpMV) strains from Spartina spec. and from Cynodon dactylon to other
members of the Potyviridae.";
Arch. Virol. 147:379-391(2002).
EMBL; AF491352; AAM12550.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8QHV1;
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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InterPro; IPR007094; RNA_pol_PSvir.
Pfam; PF00767; Poty_coat; 1.
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Last annotation update)
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Pred. No.
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., HowLand T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Harris M.L., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeb R.,-F., Zaveri J.S., Zhan M., Zhang G., Zhoo Q., Zheng L.,
RA Cheng X.H., Zhong F.N., Rubin G.M., Venter S., Shu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Stringer C. 287:2185-2195(2000)
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Best Local S
Matches 5
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InterPro; IPR003006; Ig_MHC.

InterPro; IPR007087; Znf C2H2.

Pfam; PF00096; zf-C2H2; 5.

SMART; SM00355; ZnF C2H2; 5.

PROSITE; PS00029; IG_MHC; 1.

PROSITE; PS00029; ZINC_FINGER_C2H2_1; 5.

PROSITE; PS00028; ZINC_FINGER_C2H2_2; 5.

PROSITE; PS50157; ZINC_FINGER_C2H2_2; 5.
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01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                Q8MT85
   Stapleton M., Brokstein P., Hong L., Agbayani
Champe M., Chavez C., Dorsett V., Dresnek D.,
George R., Gonzalez M., Guarin H., Kronmiller
                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                        GM13256p.
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                                                         SEQUENCE FROM N.A.
                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                          CG7861
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Yu C., Lewis S.E., Rubin
                                                                                           NCBI_TaxID=7227;
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Metal-binding;
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                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brokstein P., Hong L., Agbayani A., Carlson J., lavez C., Dorsett V., Farfan D., Frise E., George R., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., leb J., Paragas V., Park S., Phouanenavong S., Wan K S.E., Rubin G.M., Celniker S.,
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62.5%;
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Pred. No.
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RESULT 14
Q9V9K0
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AC Q9V9K
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FilyBase; FB9R0033055; CG7861.
Interpro; IPR000938; CAP-Gly.
Pfam; PF01302; CAP GLY; 1.
PROSITE; PS50245; CAP GLY 2; 1.
SEQUENCE 523 AA; 59393 MW; 4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U1-MAY-1997 (TrEMBLrel. 03, Created)
01-WAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 60.9 kDa protein.
F47F6.3.
 Q9V9K0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patel S., Ph
Celniker S.;
                                                                                                                                                                                                                    "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; U80838; AAC71112.1;
WormPep; F47F6.3; CE10708.
                                                                                                                                                                                                                                                                                                                    Wilson R., Favello A., Maggi L., Chiapelli B.; "The sequence of C. elegans cosmid F47F6."; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                     InterPro; IPR002656; Acyl transf_3. Pfam; PF01757; Acyl transf_3; 1. Hypothetical protein.
SEQUENCE 527 AA; 60919 MW; 1845
                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          investigating biology. The C
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
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                                                                                                                                                                                                                                                                      Waterston R.;
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             PRELIMINARY;
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85.7%;
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75.0%;
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Pred. No. 1.9e+02;
             PRT;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gebalos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Godson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Godson K., Doup L.B., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A Harris N.I., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
A Harris N.I., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Jalaii M., Kalush F., Karpen G.H., K. Z., Kennison J.A., Ketchman K.,
A Harris N.I., Modira C.D., Kraft C., Kraviz S., Kulp D., Lai Z.,
A Harris N.I., Modira C.D., Kraft C., Kraviz S., Kulp D., Lai Z.,
A Harris N.I., Molishina N.V., Mobarry C., Morris J., Moshreti A.,
A Weinlich B.E., Kodira C.D., Kraft C., Kraviz S., Kulp D. Lai Z.,
A Malley G., Milshina N.V., Mobarry C., Morris J., Wesheer F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Jand X.H., Shon S., Zhan M., Shang G., Zhao Q., Zheng L.,
RA Jand X.H., Shang G., Zhao Q., Zheng L.,
RA Jand X., Smith H.O.,
RA Jand X., Jand J.,
                                                                                          Query Match
Best Local
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                                                                                                                                                EMBL; AE003784; AAF57288.2; -.
FiyBase; FBgn0033055; CG7861.
InterPro; IPR00938; CAP-GBly.
InterPro; IPR001611; LRR.
Pfam; PF01302; CAP-GLY; 1.
Pfam; PF005105; LRR; 1.
PF00SITE; PS50245; CAP-GLY 2; 1.
PROSITE; PS50245; CAP-GLY 2; 1.
PSCQUENCE 542 AA; 6T580 MW; 6
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01-MAR-2001 (TrE
01-OCT-2002 (TrE
CG7861 protein.
CG7861.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=BERKELEY;
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95 NYDSSNV 101
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                                                                        6; Conserv
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85.7%;
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Last annotation updat
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RESULT 15 Q95XY3 ID Q95XY3

PRELIMINARY;

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Search completed: January 12, 2004, 07:02:17 Job time: 20.25 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AC024805; AAK39343.1; -.
WormPep; Y51H7C.12; CE26148.
InterPro; IPR005069; DUF271.
Pfam; PF03407; DUF271; 1.
Hypothetical protein.
SEQUENCE 557 AA; 64096 MW; A84DOCEAF9D247FF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 64.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRALM=Bristol N2;
Bradshaw-Cordum H., DuBuque T.;
"The sequence of C. elegans cosmid Y51H7C.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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RNGBI_TaxID=6239;
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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39
1 SYDSSNVV 8
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| SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1985_DAT:
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                 SUMMARIES
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Anti-adipocyte mon	AAU02522	22		82.1	32	9
Anti-GD2 antibody	AAO18434	23		82.1	32	œ
Drosophila melanog	ABB65449	22	1945	84.6	33	7
Arabidopsis thalia	AAG29581	21		. 84.6	33	6
Arabidopsis thalia	AAG29582	21		84.6	33	տ
Osteogenic protein	AAR60578	15		89.7	35	4
Human colon cancer	AAG76011	22		100.0	39	ω
Human TANGO 268 VL	ABU11264	24	8	100.0	39	N
Anti-TANGO 268 scF	AAB61298	22	œ	100.0	39	Þ
Description	ID	:	Match Length DB	Match	Score	No.
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45	44	43	42	41	40	39	38	37	36	35	34	LJ LJ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
30	30	30	30	30	30	30	30	31	31	31	31	<u>3</u> 1	31	31	31	31	31	31	31	31	31	31	31	31	31	32	32	32	32	32	32	32	32	32	32
76.9	76.9	76.9	6	76.9	76.9	٥,	76.9	9	9	79.5	9.	9.	9.	9	9.	9.	9.	9	۰.	9	9	9	9	9	9	ν.	2	٥.	82.1	82.1	82.1	82.1			82.1
354	352	341	308	284	126	29	18	1627	964	907	876	862	783	595	469	447	398	395	325	272	245	220	192	131	98	1938	1938	893	798	542	521	395	363	174	166
23	22	22	21	22	19	13	24	23	18	22	23	23	23	23	12	23	23	23	20	22	10	14	22	22	24	20	17	17	20	22	22	22	22	22	22
ABB92259	ABB58931	AAU68573	AAG49677	ABG16400	AAW64528	AAR22106	ABU03437	ABB98127	AAW32619	ABB62889	ABB91479	ABP35634	ABB92054	ABJ05497	AAR15510	ABP29684	ABP25919	ABP25918	AAY02465	ABB66563	AAP90386	AAR42340	ABB69449	ABB62470	ABP56510	AAW73553	AAW09255	AAW09257	AAW73552	ABB58491	ABB61042	AAE09784	AAE09791	AAE09790	AAE09787
	Drosophila melanog			Novel human diagno	lomaviz	Peptide 3-29 deriv	Human expressed pr	Human PMMM Incyte	Cyclic-isomaltolig	Drosophila melanog	Herbicidally activ	Fungal ZBC protein	idal]	Human breast cance				8		melano				Drosophila melanog	n anti-		Bacillus alkaline	Bacillus alkaline	Pullulanase protei		Drosophila melanog	lus			Paenibacillus pabu

ALIGNMENTS

RESULT 1 AAB61298

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AAB61298;

AAB61298 standard; Peptide; 8 AA.

XXX	PR	PR	PR	×	ΡF	×	В	×	PN	×	80	ğ	X	Š	ξ	ξ	Ş	ξ	Š	×	DΕ	×	ဌ
(MILL-) MILLENNIUM PHARM INC.	14-FEB-2000; 2000US-0503387.	06-DEC-1999; 99US-0454824.	30-JUN-1999; 99US-0345468.		30-JUN-2000; 2000WO-US18152.		04-JAN-2001.		WO200100810-A1.		Homo sapiens.		cancer.	ischaemia; cardiovascular disease; immunological disease; liver disorder;	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;	platelet membrane glycoprotein receptor; bleeding disorder;	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;	TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;	Human; antibody; scfv; CDR; complementarity determining region;		Anti-TANGO 268 scrv CDR, SEQ ID NO: 66.		04-APR-2001 (first entry)

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RESULT 2
ABU11264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent acture cardiac ischaemia following angioplasty and metastatic cancers,
                                                                                                                                                                                                                                                    Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboembolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; cardiovascular disease; angina pectoris; myocardial infarction; coronary restensis; atherosclerosis; immunological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, trand diagnosing hemorrhagic disorders, thrombotic diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Busfield SJ, Ville Qian MD, Kingsbury
                                                09-APR-2001; 2001US-0829495.
                                                                                                                                                     WO200280968-A1
                                                                                                                                                                                                                        cerebral vascular disease; venous thromboembolism disease
                                                                                                                                                                                                                                         developmental disorder; embryonic disorder; liver disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU11264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU11264 standard; Peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and diagnosing hemorrhagic immunological disorders -
                                                                                  09-APR-2002; 2002WO-US11122
                                                                                                                    17-OCT-2002
              (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 268 VLCDR1 Peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence is given in a specification relating to an isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             following angioplasty and colon and liver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 39; DB 22;
100.0%; Pred. No. 9.3e+05;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jandrot-Perrus M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 8;
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Sequence

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This invention relates to a novel purified antibody comprising a CC variable heavy (VH) complementarity determining region (CDR1), VH CDR2 (CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and CC immunospecifically binding to a TANCO 268 (also referred as glycoprotein CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or CC blagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration, CC morphology, differentiation and/or function of megakaryocytes and CC platelets, including during development e.g. embryogenesis, modulating platelet and platelet-endothelium interactions in CC inflammation and/or thrombosis, and modulating platelet aggregation and CC inflammation and/or thrombosis, and modulating platelet proliferation, migration, are also useful for modulating platelet proliferation, cC migration, morphology, differentiation and/or platelet proliferation, cC migration, morphology, differentiation and/or function, e.g. bleeding CC diseases such as thrombocytopaenia. Other diseases which may be CC modulated by these antibodies are thrombotic disorders, cerebral CC vascular diseases involving leg swelling, pain and ulceration, CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular CC restenosis, atheroscese involving leg swelling, pain and ulceration, coronary cretenosis, atherosceses involving leg swelling, pain and ulceration, coronary cretenosis, atherosceses involving leg swelling cardiovascular developmental disorders, embryonic disorders, liver disorders, cerebral cardiovascular final disorders, cerebral thromboembolism diseases, venous thromboembolism disease, coronary diseases, creability causes a manual disorders. The antibodies of the invention only causes a manual cardiovascular in nlatelet counts, blatelet aggregation, and/or and/or manual or nlatelet counts. Datelet aggregation, and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
                                                                               transient decrease in platelet counts, platelet aggregation, and/or platelet activation and so have some advantages over prior art methods. The present sequence represents a peptide sequence used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Busfield SJ, Villeval J, Qian DM, Kingsbury G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                       generate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 111;
                                                          antibodies of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jandrot-Perrus M,
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RRSULT 3
AAG7601
ID AAG77
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Best Local
                                                                                                                                                                                                                                                                                                                                                          Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 22.
    28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human colon cancer antigen protein SEQ ID NO:6775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG76011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG76011 standard; Protein;
                                                                                            05-APR-2001.
                                                                                                                                                                                    WO200122920-A2
                                                                                                                                                                                                                                                                       Homo sapiens
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8; Conser
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RESULT 4
AAR60578
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAH35416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1999;
03-NOV-1999;
                                                                                                 Cleavage-site
                                                                                                                                                                                                    Osteogenic protein.
                                                                                                                                                                                                                               Osteogenic protein OP2.
                                                                                                                                                                                                                                                               25-MAR-2003
30-MAR-1995
                                                                                                                                                                                                                                                                                                          AAR60578;
                                                                                                                                                                                                                                                                                                                                      AAR60578 standard; Protein; 402 AA
 04-MAR-1994;
                            15-SEP-1994.
                                                        WO9420539-A1
                                                                                                                            Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-235357/24.
                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                             114 SYDSSNVV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 SYDSSNVV 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161
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                                                                                                                                                                                                                                                              (updated)
(first entry)
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99US-0163280.
94WO-US02335.
                                                                                                                            Location/Qualifiers
239..242
                                                                                                   /note= "proteolytic cleavage site"
260..263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                     "proteolytic cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2
Pred. No. 1.9;
0; Mismatches
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RESULT 5
AAG29582
ID AAG2
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Best Local
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05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-WAR-1999
06-APR-1999
06-APR-1999
16-APR-1999
11-APR-1999
21-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cultures, and may be provided to a site for bone induction in a mammal with a suitable matrix to allow infiltration, proliferation and differentiation of migrating progenitor cells. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones WK,
Tucker RF
                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                  17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                       AAG29582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 50-52; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ71426
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                                                                                                                                                                                                                                                Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 35222.
                                                                                                                                                                                                                                                                                                                                                                          AAG29582 standard;
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99US-0125788.
99US-0126785.
99US-012762.
99US-0127762.
99US-0127762.
99US-0128734.
99US-0130077.
99US-0130077.
99US-0130610.
99US-0130610.
99US-013048.
99US-013048.
                                                                                                                                            99US-0121825.
99US-0123180.
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99US-0128714

99US-0130477

99US-013049

99US-013049

99US-013149

99US-0132485

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99US-0145913.
99US-0145918.
99US-0146388.
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99US-0147204.
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99US-0151080.
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                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and interactions -
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N-PSDB; ABL09552.
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11-JUL-2000; 2000US-0614150
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                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ
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                                                                                                                                                                                                                                                             The present invention relates to a composition for treating tumours positive for disialoganglioside GD2 which is based on human antibody fragments that activate the immune system against GD2, specifically by inducing anti-GD2 antibodies. The composition can be used in the treatment of neuroblastoma and melanoma. The present sequence is an
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DE10059930-A1
                                           29-AUG-2001
                                                                 AAU02522;
                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 7A; 14pp; German
                                                                                                                                                                                                                                                                                                                                                               Composition for treating tumors that produce disialoganglioside GD2, comprises human antibody fragment able to induce anti-idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-510006/55
                                                                                                                                                                                                                                                                                                                                                                                                                      Uttenreuther-Fischer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-NOV-2000; 2000DE-1059930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-NOV-2000; 2000DE-1059930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 melanoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-GD2 antibody light chain #11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAO18434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAO18434 standard; protein; 110
Antibody; adipocyte; heavy chain; light chain; obesity; fat;
                    Anti-adipocyte monoclonal antibody light chain, FAT 13
                                                                                     AAU02522 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (FISC/) FISCHER P. (UTTE/) UTTENREUTHER-FISCHER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-GD2 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1266 ŚYEŚŚNII 1273
                                                                                                                                           91
                                                                                                                                                                 1 SYDSSNV 7
                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                           SYDSSNL 97
                                                                                                                                                                                                                                                    antibody light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYDSSNVV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccine;
                                                                                                                                                                                                                                 110 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               neuroectodermal tumour; cancer; neuroblastoma. gene therapy; cytostatic; disialoganglioside (
                                                                                      Protein;
                                                                                                                                                                                               82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Krueger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ω
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                                                                                                                                                                                     1;
                                                                                                                                                                                     Score 32; DB Pred. No. 38; 1; Mismatches
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                                                                                                                                                                                                         23;
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                                                                                                                                                                                                         Length 110;
                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GD2
                                                                                                                                                                                    Gaps
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RESULT 10
AAE09787
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease.
                                   Xyloglucanase; XYG1035; glycosyl hydrolase; textile industry; detergent; cellulose fibre; hemp; jute; flax; linen; garment manufacture.
                                                                                                                                        29-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 106; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS03422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards BM, Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-OCT-2000; 2000WO-GB03900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heart disease; complementarity determining region; CDR
Paenibacillus pabuli
                                                                                                Paenibacillus pabuli xyloglucanase XYG1035 enzyme C-terminal sequence.
                                                                                                                                                                                   AAE09787;
                                                                                                                                                                                                                      AAE09787 standard; Protein; 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200127279-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001-282031/29.
                                                                                                                                                                                                                                                                                                                           95
                                                                                                                                                                                                                                                                                                                                                           SYDSSNVV 8
                                                                                                                                                                                                                                                                                                                           SYDSSNRV 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                            82.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaughan TJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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39;
                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 113;
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07-SEP-2001

WO200164853-A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches: 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel xyloglucanase enzyme for use in textile, fiber processing industries comprises family 5 and is derived from strains of Paenibacillus -
WPI; 2001-565502/63.
                             Wilting R, Bjornvad ME,
                                                                                            01-MAR-2000; 2000DK-0000326
                                                                                                                                                            07-SEP-2001
                                                                                                                                                                                                                        Paenibacillus pabuli.
                                                                                                                                                                                                                                                     Xyloglucanase; XYG1037; glycosyl hydrolase; textile industry;
cellulose fibre; hemp; jute; flax; linen; garment manufacture.
                                                                                                                                                                                                                                                                                                       Paenibacillus
                                                                                                                                                                                                                                                                                                                                     29-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                   AAE09790 standard; Protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 91-92; 99pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-565502/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilting R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2000; 2000DK-0000326
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                                                                                                                           28-FEB-2001; 2001WO-DK00132.
                                                              (NOVO ) NOVOZYMES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۳,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYDSSNIV 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYDSSNVV 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bjornvad ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                       pabuli xyloglucanase XYG1037 enzyme C-terminal sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.1%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kauppinen MS,
                             Kauppinen MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schuelein
                                Schuelein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            detergent and cellulose of glycosyl hydrolases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                         detergent
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                         AAE09791
                                             RESULT 12
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                                                                                                                                                                                                                   Best Local
Matches
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel xyloglucanase enzyme for use in textile, detergent and cellulose fiber processing industries comprises family 5 of glycosyl hydrolases and is derived from strains of Paenibacillus -
                                                                                                                                                                                                                                                                                                              Sequence
AAE09791 standard; Protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
                                                                                                                                                                                                                                                                                                                                                                conventional liquid
                                                                                                                      117 SYDSSNNV 124
                                                                                                                                                                   1 SYDSSNVV
                                                                                                                                                                                                                   Similarity 7; Conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                   174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 93; 99pp; English.
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                   æ
                                                                                                                                                                                                                                                                                                                                                                detergent
                                                                                                                                                                                                                                            82.1%;
87.5%;
                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                            Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                compositions.
                                                                                                                                                                                                                     Mismatches
  Ą
                                                                                                                                                                                                                                               DB
64;
                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                     1;
                                                                                                                                                                                                                                                                   Length 174;
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                                                                                                                                                                                                                     Gaps
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Xyloglucanase; XYG1034; glycosyl hydrolase; textile industry; detergent;
cellulose fibre; hemp; jute; flax; linen; garment manufacture.
07-SEP-2001.
                                                                                                                                                                                                                                                                            29-NOV-2001
                                            WO200164853-A1
                                                                                              Paenibacillus pabuli.
                                                                                                                                                                                                                       Paenibacillus pabuli mature
                                                                                                                                                                                                                                                                                                                           AAE09791;
                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                       xyloglucanase XYG1034 enzyme
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01-MAR-2000; 2000DK-0000326

(NOVO ) NOVOZYMES

28-FEB-2001; 2001WO-DK00132

Novel xyloglucanase enzyme for use in textile, fiber processing industries comprises family 5 and is derived from strains of Paenibacillus

detergent and cellulose of glycosyl hydrolases

N-PSDB; AAD16819. WPI; 2001-565502/63. Wilting R,

Bjornvad ME,

Kauppinen MS,

Schuelein

Example 7;

Page

95;

99pp;

English

The present sequence is Paenibacillus pabuli xyloglucanase XYG1034

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RESULT 13
AAE09784
ID AAEC
XX AAE
AC AC
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CC Xyloglucanase is useful for machine treatment of fabrics during a washing CC cycle of a machine washing process with a washing solution. Xyloglucanase is useful in textile industry for improving the properties of cellulosic CC fibres, yarn, woven or non-woven fabric and in scouring process step, in CC cellulose fibre processing industry for ratting of fibres such as hemp, in CC cycle, flax and linen. Xyloglucanase is useful for treatment of cellulosic CC material during the processing of cellulosic material into a material CC ready for garment manufacture or fabric manufacture, e.g. in the desizing CC or scouring or during industrial or household laundering of such fabric CC or garment. Xyloglucanase is also useful in detergent compositions for CC removing or bleaching certain soils or stains present on laundry, CC especially soils and spots resulting from xyloglucan-containing food and plants. Xyloglucanase prevents binding of certain soils to the xyloglucan containing food and left on the cellulosic material and shows high performance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 7
                                                                                                                                                             Novel xyloglucanase enzyme for use in textile, fiber processing industries comprises family 5 and is derived from strains of Paenibacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conventional liquid detergent compositions.
                                                                                                                                                                                                                                                                                                   WPI; 2001-565502/63.
N-PSDB; AAD16817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2000; 2000DK-0000326.
                                                                                                  Claim 3; Page 88-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2001; 2001WO-DK00132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200164853-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycosyl hydrolase family 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xyloglucanase; XYG1009; glycosyl hydrolase; textile industry; detergent; cellulose fibre; hemp; jute; flax; linen; garment manufacture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Paenibacillus pabuli xyloglucanase XYG1009 enzyme.
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. 1.5e+02;
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The present sequence enzyme which belongs

to 18

Paenibacillus pabuli xyloglucanase XYG1009 the family 5 of glycosyl hydrolases.

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RESULT 14
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Best Local !
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                     capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-656860/75.
N-PSDB; ABL05145.
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Pred. No.
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ABB58491
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Best Local Similarity
Matches 6; Conserva
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                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                           The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                        New isolated nucleic a
genes from Drosophila
interactions -
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N-PSDB; ABL02594.
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                                                                                                     Sequence
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11-JUL-2000; 2000US-0614150.
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3; Mismatches 0
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Search completed: January 12, 2004, 06:58:59 Job time : 21.375 secs

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Post-processing: Minimum Match 0%
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106.117 Million cell updates/;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

					COLUMNICATION	
Result No.	Score	Query Match	Length	BB	ID	Description
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2	34	89.5	109	_	L1HUWA	chain
ω	34		111	ب	LIHUNW	lambda chain
4	34	89.5	131	μ	L6HUEB	lambda chain
ភ	34	•	266	N	S72947	pothetical pro
9	34		704	N	T02558	cal
7	33	•	111	<b>1-3</b>	L6HULT	chai
8	32		111	<u></u>	L6HUST	lambda
9	32		460	N	T27770	hypothetical prote
10	32	•	471	N	T20690	hypothetical prote
11	32		603	N	AC0674	probable glycogen
12	31		107	N	PC4283	anti-SS-A/Ro 60K p
13	31	81.6	161	N	E81447	anscriptio
14	30	٠	108	<u> </u>	L5HUDL	
, <u>, ,</u> 5	30	٠	158	N	C95159	
16	30	٠	158	N	C98025	shikimate kinase (
17	30	٠	232	N	C84706	probable small nuc
18	30		332	N	A45710	BRRF2 gene homolog
19	30	•	361	٧	T30402	hypothetical prote
20	30	٠	371	Н	E64821	yliI protein precu
21	30	•	371	N	4	probable dehydroge
22	30	•	371	N	59	probable dehydroge
23	30	•	420	N	B86217	protein T27G7.4 [i
24	30	8	462	_	S35534	adenovirus ElA enh
25	30	78.9	522	N	D82195	icat
26	30	8	555	بر	S24061	cription
27	30		620	ب	833253	protein-tyrosine k
28	30	78.9	664	N	T01368	hypothetical prote
29	30	78.9	885	μ	A55453	nucleotide diphosp

44 1	43	42	41	40	9	38	37	36	35	34	33	32	31	30
29	29	29	29	29	· 29	29	29	29	29	29	29	29	29	29
76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3	76.3
318	312	243	232	202	202	202	202	195	132	117	112	111	106	98
20	<b>у</b> Р	ผ	N	۳,	μ	μ	Н	N	2	N	N	N	N	N
H69959	S22397	A96744	S25742	MEVNINA	MEVNCV	MEVNAV	MFVNRV	A27241	I39004	S04525	S51125	S47009	S38495	836068
hypothetical prote	pyruvate synthase	hypothetical prote	Ig lambda chain -	matrix protein - r	helix-destabilizin	cyclin-dependent k	Ig lambda chain pr	genome polyprotein	Ig lambda chain V1	Ig lambda chain -	Ig lambda chain -			

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C;Generucs:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: amyloid; heterotetramer; immunoglobulin
F;15-93/Domain: immunoglobulin homology <IMM>
F:32-91/Disulfide bonds: #status predicted
                                                                                                                                          Ig lambda chain V-I region (Wah) - human
(;Species: Homo sapiens (man)
(;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 02-Sep-1997
(;Accession: A01967
R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.
Proc. Natl. Acad. Sci. U.S.A. 80, 3686-3690, 1983
A;Title: Complete covalent structure of a human immunoglobulin D: sequence A;Reference number: A01967; MUID:83221661; PMID:6407018
A;Accession: A01967
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Biochem. J. 195, 561-572, 1981
A;Title: The complete amino acid sequence of a prototype immunoglobulin-lambda light-cha
A;Reference number: A01987; MUID:82091000; PMID:6797401
A;Contents: amyloid protein AR
A;Accession: A01987
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c;Species: Homo sapiens (man)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 31-Mar-2000
C;Accession: A01987
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A; Residues: 1-112 <SLE>
A; Residues: 1-112 <SLE>
C; Comment: This protein was isolated from the spleen of a patient with amyloidosis.
                         C;Genetics:
A;Gene: GDB:IGLV@
                                                                                        A; Molecule type: protein A; Residues: 1-109 < TAK>
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A;Cross-references: GDB:119342; OMIM:147240
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Best Local :
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85.7%; Pred. No. 2.2;
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Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A;Title: The complete amino acid sequence of Bence-Jones protein
A; Reference number: A01964; MUID:69060892; PMID:4177823
A; Accession: A01964
A; Molecule type: protein
A; Residues: 1-111 < LAN>
C; Gement: This is a Bence Jones protein.
C; Genetics:
                                                                                                                        A,Title: Cloning and sequence analysis of an Ig lambda light chain mRNA expressed A,Reference number: A01990; MUID:85215660; PMID:3923440

A,Rocession: A01990

A,Molecule type: mRNA
A,Residues: 1-131 <AND>

C;Genetics:
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A;Gene: GDB:IGIV@

A;Cross-references: GDB:119342; OMIM:147240

A;Map position: 22q11.2-22q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
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                                                                                                                                                                                                                                                               R;Anderson, M.L.M.; Brown, L.; McKenzie, Nucleic Acids Res. 13, 2931-2941, 1985
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A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer
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Best Local S
Matches 6
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                                                                                                                                                                                                                                                                                                           g lambda chain precursor V-VI region (EB4) - human
;Species: Homo sapiens (man)
;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997;Accession: A01990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 24-Nov-1999
Accession: A01964
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6; Conserv
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    Mismatches

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Pred. No. 3
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Pred. No. 3.
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3.6;
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3.5;
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hypothetical protein At2g32590 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T26815.15
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 02-Feb-2001
C;Accession: T02558; A84735
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.;
submitted to the EMBL Data Library, July 1998
A;Description: Arabidopsis thaliana chromosome II BAC T26B15 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: $72947
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library,
A;Description: Mycobacterium leprae
A;Reference number: $72587
A;Accession: $72947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein B2235_F2_77 - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #Bequence_revision 25-Apr-1997 #text_change
C;Accession: S72947
R;Smith, D.R.; Robison, K.
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: A84735
                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-704 <ROU>
A;Cross-references: EMBL:AC004681; NID:g3298532; PID:g3298547
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F;70-76/Region: complementarity-determining
F;77-110/Region: framework 3
                                                                                                 A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S. D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.;
R;Lin, X.; Kaul, S.; Rounsley, S. D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Pujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, v
                                                                                                                                                                                                                                                                                                   A; Reference number: Z14678
A; Accession: T02558
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A; Residues: 1-266 < SMI >
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      k; Score 34; DB
k; Pred. No. 8.8
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34; DB 1; ; Pred. No. 4.3; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    K.A.; Crosby, M.L.; Brandon, R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EB4) #status predicted <MAT>
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Sykes,

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Query Match
Best Local Similarity
Watches 6; Conserva
                                                                                                                                                    Ig lambda chain V-VI region (SUT) - human
(;Species: Homo sapiens (man)
(;Species: Homo sapiens (man)
(;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
(;Accession: A01988
R;Solomon, A.; Kyle, R.A.; Frangione, B.
in Amyloidosis, Glenner, G.G., Osserman, E.F., Benditt, E.P., Calkins, E., in A;Title: Light chain variable region subgroups of monoclonal immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Keywords: heterotetramer; immunoglobulin F;1-22/Region: framework 1 F;15-93/Domain: immunoglobulin homology <IMM>F;23-35/Region: complementarity-determining 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: A01989

R;Dwnlet, F.E.; Strako, K.; Benson, M.D.
Scand. J. Immunol. 22, 653-660, 1985
A;Title: Amino acid sequence of a lambda VI primary (AL)
A;Reference number: A01989; MUID:86122667; PMID:4089539
A;Accession: A01989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig lambda chain V-VI region (WLT) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
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A;Residues: 1-704 <STO>
A;Cross-references: GB:AE002093; NID:g3298547; PIDN:AAC25941.1; GSPDB:GN00139
                                          A; Molecule type: protein A; Residues: 1-111 < SOL> C; Genetics:
                                                                                                            A; Reference number: A01988
A; Accession: A01988
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A;Residues: 1-111 <DWU>
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A;Cross-references: GDB:119342; OMIM:147240
                                                                                                                                                                                                                                                                                                                                         RESULT 8
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Best Local S
Matches 6
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                         ;Gene: GDB:IGLV@
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:22-91/Disulfide bonds:
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85.7%;
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Pred. No.
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Pred. No.
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                                                                                                                                                                              A.S.,
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A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-471 <WIL>
                                                                                                                                                              submitted to the EMBL Data Library, February 1995
A;Reference number: Z19310
A;Accession: T20690
                                                                                                                                                                                                                                                   hypothetical protein F1085.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T20690
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C;Superfamily: Caenorhabditis elegans hypothetical protein ZK177.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-460 <AND>
A;Residues: 1-460 <AND>
A;Cross-references: EMBL:U21321; PIDN:AAB36965.1; GSPDB:GN00020; CESP:ZK177.1
A;Experimental source: strain Bristol N2; clone ZK177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z20416
A; Accession: T27770
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C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                   R;Sims, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein ZK177.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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                                                          A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                            T20690
                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: ZK177.1
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A;Description: The sequence of C. elegans cosmid ZK177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Anderson, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
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A; Map position:
                    A;Gene: CESP:F10B5.3
                                                                                A;Cross-references: EMBL:Z48334; PIDN:CAA88310.1; GSPDB:GN00020; CESP:F10B5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 2
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Best Local S
Matches 6
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Best Local
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Pred. No.
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9.8;
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A; Molecule type: protein A; Residues: 1-107 <SUZ> C; Comment: This antibody i C; Superfamily: immunoglobu F; 13-87/Domain: immunoglob
                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change
C;Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change
C;Accession: PC4283
R;Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi,
Biochem. Biophys. Res. Commun. 232, 101-106, 1997
A;Title: Molecular cloning of anti-ss-A/Ro 60-459
A;Reference number: PC4279; MUID:97236289; PMID:9125110
A;Accession: PC4283
                    RESULT 13
E81447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: STY1505
C;Superfamily: glyX protein
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AC0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable glycogen debranching protein (EC 3.2.1.-) [imported] - Salmonella (C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AC0674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
AC0674
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transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-603 < PAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns:
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Best Local (
                                                                                                                                                                                                                                                Comment: This antibody is commonly found in systemic; Superfamily: immunoglobulin V region; immunoglobulin; 13-87/Domain: immunoglobulin homology <IVM>
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Best Local (
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  factor Cj0287c [imported] - Campylobacter jejuni (strain
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85.7%;
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Pred. No.
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Pred. No.
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Pred. No. 15;
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homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.; Wain, J.; Churcher, L.; White, N.; Farrar
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C95159
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                    C;Accession: C95159
C;Accession: H:; Nelson, K.E.; Paulsen, I.T.;
on, J.D.; Umayam, L.A.; White, O.; Salzberg,
nson, T.; Hickey, E.K.; Holt, I.E.
                                                                            C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision
C;Accession: C95159
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                                                                                                                                      shikimate kinase [imported] -
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293,

498-506,

pneumoniae

Streptococcus pneumoniae (strain TIGR4)

03-Aug-2001

#text_change

24-Aug-2001

Eisen, J.A.; S.L.; Lewis,

J.A.;

Read,

T.D.; Peterson, S.; Her Padune. D.; Holtzapple,

Hei

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A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: greA; Cj0287c
C;Superfamily: transcr
C;Keywords: transcript
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-
C;Accession: E81447
C;Accession: E81447
R;Parkhill, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.;
Nature 403, 665-668, 2000
Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 1-108 <EUL>
A; Note: this is the first s
C; Comment: This is a Bence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig lambda chain V-V region (Del) -
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revis
C;Accession: A01985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72754.1; PID:g696776
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyph;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: E81447
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: A01985
                                                                                                                                                              F;14-88/Domain: immunoglobulin homology <IMM>F;21-86/Disulfide bonds: #status predicted
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C; Comment: This
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                                                                                                 Query Match
Best Local
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Best Local
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tle: A new subgroup of human L-chains of the lambda-type.
ference number: A01985; MUID:75112179; PMID:4452363
48 EDNDRPA
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Jones protein.
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Pred. No.
                                                                                                   Score 30;
Pred. No.
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A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A,Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; pMID:11463916

A;Accession: C95159
A;Accession: C95159
A;Accession: C95159
A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-158 «KUR»
A;Residuse: 1-158 «KUR»
A;Reperimental source: strain TIGR4
C;Genetics:
A;Gene: SP1370
C;Superfamily: shikimate kinase; shikimate kinase homology
Query Match
Best Local Similarity 83.3%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNQRP 6
Db 109 KDNQRP 114
Search completed: January 12, 2004, 07:03:07
Job time: 9.34375 secs

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OM protein -

protein search,

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen

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January 12, 2004, 06:47:49 ;

; Search time 3.82812 Seconds
(without alignments)
85.992 Million cell updates/sec

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LVIF HUMAN
ID LVIF HUMAN
AC P04208;
DT 20-MAR-1987 (
DT 20-MAR-1987 (
DT 15-JUL-1999 (
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Best Local Similarity
Matches 6; Conserv
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HSSP; P01709; 2MCG.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0003823; F:antigen binding activity; NAS.

G0; G0:0006955; P:immune response; NAS.

InterPro; IPR003106; Ig_MHC.

InterPro; IPR003106; Ig_v.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGV; 1.

SMART; SM00406; IGV; 1.

Inmunoglobulin V region; Amyloid.

DOMAIN

1 107 IG-LIKE.
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NON_TER
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Sletten K., Natvig J.B., Husby G., Juul J.;
"The complete amino acid sequence of a prototype
immunoglobulin-lambda light-chain-type amyloid-fibril protein AR.";
Biochem. J. 195:561-572(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
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P01721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATIENT WITH AMYLOIDOSIS.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM THIS PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig lambda chain V-VI region AR.
                                                                                                                                                                              51
                                                                                                                                                                                                                 1 EDNORPS 7
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                                                                                                                                                                                                                                                                                                                                        112 AA; 11918 MW; 570BCD9A368EF1FE CRC64;
  (Rel.
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5376
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                                                                                                                                                                                                                                                        92.1%; Score 35; DB 1;
85.7%; Pred. No. 0.73;
:ive 1; Mismatches
                                       Created)
  Last sequence update)
Last annotation update)
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YDVB_SCHPO
SYA_AQUPY
ORCI_DROME
PHYA_SORBI
RA16_SCHPO
DPOL_ADE04
V120_EBV
V120_HUMAN
POLG_HUMAN
POLG_HUWB
ZAN MOUSE
VXIS_BPMD2
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O14226
Q9xdm3
Q9xdm3
O16810
P93526
P53692
P87503
P071118
P07210
O88799
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homo sapien
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drosophila
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schizosacch
                                                                                                                                                                                                                                                          Gaps
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Result No.

Score

Query Match Length DB

NPP2_MOUSE NPP2_RAT ROA1_BOVIN

ETV4 HUMAN ETV4 MOUSE

ECOLI

Q02484 P75804

homo sapien

ij

HUMAN

LV6C_HUMAN YS41_CAEEL GREA_CAMJE

LV5A_HUMAN YIE2_HSVB4

LV6D_HUMAN PEA3_BRARE

Q9puq1 P06317 Q9pik9 Q09370

9 homo sapien
8 homo sapien
1 brachydanio
7 homo sapien
0 caenorhabdi
9 campylobact
9 homo sapien
4 bovine herp
4 escherichia

P06318

P06319 P01701

homo

homo sapi sapien

LV1F_HUMAN LV1C_HUMAN LV6E_HUMAN

TARMOH TABAT

Description

VMAT_RABVA
VMAT_RABVC
VMAT_RABVY
VMAT_RABVN
VMAT_RABVN
VMAT_RABVP
VOHQ_BACSU
ROA1_MACMU
ROA1_MOUSE

P243268 P243262 Q08881 Q08881 Q971e6 Q64610 P09867 P15200 P13512 P135124 P25224 P25224 P25224 P25224 P35224 P3524 P35224 P35224 P35224 P35224 P35224 P35224 P35224 P35224 P35224

1 homo gapien
6 m ectonucle
0 r ectonucle
7 bos taurus
7 bos taurus
7 rabies viru
8 rabies viru
1 rabies viru
1 rabies viru
1 rabies mula
2 mus musculu
6 rattus norv
1 homo sapien
6 mus musculu

ROA1_RAT ROA1_HUMAN DNPE_MOUSE

PRIG

ERWCH

ETV1_HUMAN ETV1_MOUSE ERM_HUMAN

mus musculu homo sapier

erwinia chr

Minimum Maximum

DB DB

seq

length:

2000000000

Total number of hits satisfying chosen parameters:

127863 seqs, 47026705 residues

Scoring table: Sequence: Title: Perfect score:

BLOSUM62 Gapop 10.0

Gapext 0.5

US-09-829-495-65 38

1 EDNQRPS 7

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

summaries

Database

SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 3
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Matches 6
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InterPro; IPA.
InterPro; IPR00355v.,
InterPro; IPR00355v.,
IPR0047; ig; 1.
PR0817; SM00406; IGv; 1.
R PR0SITS; PS59835; IG LIKE; 1.
R PR0SITS; PS69835; IG LIKE; IG 
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000552; P:amtigen binding activity; NA;
GO; GO:000555; P:immune response; NAS.
InterPro; IPR007110; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein;
                                                                                                                                                                                                                                                                                                                                                        MEDIINE=69060892; PubMed=4177823;
Langer B., Steinmetz-Kayne M., Hilso
"The complete amino acid sequence of
type). Subgroups in the variable par
the lambda-type.";
Hoppe-Seyler's Z. Physiol. Chem. 349
-i- MISCELLANEOUS: THIS IS A BENCE-
-i- SIMILARITY; Contains 1 immunoglo
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Homo sapiens
Bukaryota; Me
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SEQUENCE
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GO; GG
GO; GG
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21-JUL-1986 (Rel. 01, Last sequence
15-SEP-2003 (Rel. 42, Last annotatio
Ig lambda chain V-I region NEW.
Homo sapiens (Human)
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Proc. Natl. Acad. Sci.
PIR; A01967; L1HUWA.
HSSP; P01703; 7FAB.
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                                                                                                                                                                                                                                                                                                             PIR; A01964; L1HUNW. HSSP; P01703; 7FAB.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P01701;
21-JUL-1986
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MEDLINE=83221661; PubMed=6407018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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Butheria; Primates; Catarrhini; Hominidae; Homo.
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22
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         Bence-Jones protein;
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                                                                                                                                                                                                                                                                                                                                                               Chem. 349:945-951(1968).
A BENCE-JONES PROTEIN.
immunoglobulin-like doma
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e of a human
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J SEGMENT.
BY SIMILARITY.
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L; Mismatches
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Pred. No. 1.2;
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Hilschmann N.;
nnce of Bence Jones protein New (lambda-
nle part of immunoglobulin L-chains of
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STANDARD;

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RESULT 5
LV6D HUMAN
ID LV6D HUMAN
AC P06318;
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DOMAIN
DOMAIN
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DOMAIN
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SIGNAL
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=85215660; PubMed=3923440;
Anderson M.L.M., Brown L., McKenzie E., I
"Cloning and sequence analysis of an Ig :
expressed in the Burkitt's lymphoma cell
Nucleic Acids Res. 13:2931-2941(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig lambda chain V-VI region EB4 precursor.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      A01990; L6HUEB.
                                                                                                                                                                                                                                                                                                                                                             P01709; 2MCG.
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                                                            70
                                                                              1 EDNORP
                                                                                                Similarity 6; Conserv
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nilarity 85.7%;
Conservative
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20
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70
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                                                                                                                                         AA;
                                                                                                                                                                                                                                                           V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
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111
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                                                                                                                                         14147 MW;
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                                                                                                                                                                                                                                                             Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                           FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB
Pred. No. 1.2
                                                                                                                      Score 34;
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PYRROLIDONE CARBOXYLIC
BY SIMILARITY.
                                                                                                                                                                                                                     IG LAMBDA CHAIN V-VI REGION EE FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                             Pred.
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                                                                                                                                         02A9179C8C05C2CD
                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                          activity; NAS
                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131
                                                                                                                                                                                                                                          CHAIN V-VI REGION EB4
                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                           Kellow J.E., lambda light line EB4.";
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                                                                                                                    Length 131;
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                                                                                                                                           CRC64;
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chain
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Best Local S
Matches 6
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SEQUENCE.
MEDLINE=86122667; PubMed=4089539;
MEDLINE=86122667; PubMed=4089539;
Dwulet F.E., Strako K., Benson M.D.;
"Amino acid sequence of a lambda VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1988
01-JAN-1988
15-JUL-1999
                                                                                                                                                                                                 Q9PUQ1; O57586;
28-FEB-2003 (Re)
28-FEB-2003 (Re)
28-FEB-2003 (Re)
                                                                                                                                                                                                                                                                                                                                                                               DISULFID
NON TER
SEQUENCE
                                                                                                                                                                                                                                                    BRARE
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DOMAIN
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DOMAIN
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIK
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                             MEDLINE=98334393; PubMed=9671318;
Brown L.A., Amores A., Schilling
de Launoit Y., Sharrocks A.D.;
"Molecular characterisation of th
transcription factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A01989; L6HULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scand. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ig lambda chain v-vi
                                                                                                                                 Brachydanio rerio (Zebrafish)
Bukaryota; Metazoa; Chordata;
Actinopterygii, Neopterygii; T
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                      Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                       ETS-domain transcription
SEQUENCE FROM N.A.,
                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                           PEA3 BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                  SSUE=Embryo;
                                                                                                                                                                                                                                                                                              51
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                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                         EDNORPS 7
                                                                                                                                                                                                                                                                                              ENNORPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 06,
(Rel. 06,
(Rel. 38,
hain V-VI
                                                                                                                                                                                      (Rel. 41, Last sequence up
(Rel. 41, Last annotation
transcription factor PEA3.
                                                                                                                                                                                                                                                                                                                                                                                111 AA;
                                                                                                                                                                                                                   (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2MCG.
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gv; 1.
IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06, Created)
06, Last sequence up
38, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22:653-660(1985)
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35
50
57
91
101
111
111
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AND TISSUE SPECIFICITY
                                                                                                      TISSUE
                                                                                                                                                                                                                                                                                                                                                                                 11966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region WLT
                                                                                                                                                                                                                                                                                                                                                86.8%;
                                                            Schilling T.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ۳.
                                                                                                      SPECIFICITY,
                                         of the
                                                                                                                                             n) (Danio rerio).
; Craniata; Vert
Teleostei; Osta
                                                                                                                                                                                                                                                                                                                                                Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                     ΥВ
                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENTARITY-DETERMINING-3 FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENTARITY-DETERMINING-2 FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
                                                                                                                                                                                                                                                                                                                                                                                0C88B2FE37BCE24F CRC64;
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                        zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                           494
                                                                                                                                                                                              update)
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                                                            Jowett
                                                                                                                                              Vertebrata; El Ostariophysi;
                                                                                                      DNA-BINDING,
                                                                                                                                                                                                                                                                                                                                                             В
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                                         PEA3
                                                            ;
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                                                                                                                                                                                                                                                                                                                                                           Length 111;
                                                                                                                                                                                                                                                                                                                                        Indels
                                         ETS-domain
                                                             Baert
                                                                                                                                                        Euteleostomi;
                                                                                                      AND
                                                                                                                                              Cypriniformes;
                                                                                                      REGULATION
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THEFFE THE STANDARD BE READED TO SOLUTION OF THE SOLUTION OF THE STANDARD BE READED TO SOLUTION OF THE SOLUTION OF THE SOLUTION OF THE SOLUTION OF
phosphorylation.
DOMAIN 47
DOMAIN 37
DNA BIND 350
CONFLICT 148
CONFLICT 217
CONFLICT 224
                                                                                                                                                               PROSITE; PS00345; ETS DOMAIN 1; 1.
PROSITE; PS00346; ETS DOMAIN 2; 1.
PROSITE; PS50061; ETS DOMAIN 3; 1.
DNA-binding; Nuclear Protein; Acti
                                                                                                                                                                                                                                                                                                                                                                                                                         ZFIN; ZDB-GENE-990415-71; pea3.
GO; GO:0005634; C:nucleus; IZS.
GO; GO:001563; F:transcriptional activator activity; IDA.
GO; GO:0009790; P:embryonic development; NAS.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :- :-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roehl H., Nuesslein-Volhard C.; "Zebrafish pea3 and erm are general targets of FGF8 signaling."; Curr. Biol. 11:503-507(2001).
                                                                                                                                                                                                                                                                               Pfam; PF04621; ETS PEA3 N; 1. PRINTS; PR00454; ETSDOMAIN.
                                                                                                                                                                                                                                                                                                        Pfam; PF00178; Pfam; PF04621;
                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000418; Ets.
InterPro; IPR006715; ETS_PEA3_N.
InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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MEDLINE=20005800;
                                                                                                                                                                                                                                                              SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE ETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Tight transcriptional control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Raible F., Brand M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roehl H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21305906;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mech.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Binds to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Expression of the Ets transcription factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fgf signaling during early zebrafish development."; ch. Dev. 107:105-117(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Nuclear (By similarity).

TISSUE SPECIFICITY: In the embryo, expressed ubiquitously until the late blastula stage, in the marginal zone of gastrula stages, in the presumptive forebrain and hindbrain and in the trunk region of early somite stages. In later stages, also expressed in Rohon-Beard neurons, epiphysis, lateral line placodes, pectoral fin buds, developing lens and heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Phosphorylated (Probable).
MISCELLANEOUS: Transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acquisition of specific cell fates at an early stage development of the somites and nervous system. May me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embryogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cellular effects of the fibroblast growth factors on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AJ003200; CAA05980.1; -. AF168008; AAD50434.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P14921; 2STT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. 88:233-236(1999).
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OPMENTAL STAGE: First
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERK and PKA
                                                                                                                                                                                                                                                                                                                                   Ets;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By the fibroblast growth
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Ober E.A., Steinbeisser H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=11520667;
    78
430
148
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218
226
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                        ASP/GLU-RICH (ACIDIC).
ETS-DOWAIN.
A -> G (IN REF. 2).
S -> A (IN REF. 2).
ID -> MH (IN REF. 2).
    MISSING
                                                                                                                                                                 Activator; Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detected in the embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВУ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGF3
  (IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factors FGF3 and FGF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND
                 . 2).
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F. 2).
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MBL outstation -
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RESULT YS41 CA ID YS41 CA ID YS41 CA QO DT 01 DT 16 DT 16 DT Hy GN ZKK OS Ca CO CK Rh
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Best Local :
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InterPro; IPR007110; I.
InterPro; IPR003006; I.
InterPro; IPR003596; I
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                                                                                      01-NOV-1997
16-OCT-2001
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Mammalia; Eutheria;
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15-SEP-2003
                                                                        Hypothetical
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01-NOV-1997
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SMART; SM00406; IG
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"Light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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(In) Glenner G.G.,
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A.S., Zucker-Franklin D. (eds.);
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 Nematoda; Chromadorea; rinae; Caenorhabditis.
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Ig_MHC.
Ig_v.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subgroups
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
                                                                                                                                                                                                                                                                                                                                                Score 32; DB 1;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-3 FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAMEWORK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 -> MQ (IN REF. 2).
81492553EA25C362 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      0941DD547D983598 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Press, New York (1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY
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11;
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                    Rhabditida; Rhabditoidea;
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Best Local S
Matches 5
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28-FEB-2003
28-FEB-2003
                                                                                                                                                                                                                                                             MEDLINE=20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd s
Basham D., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GREA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed: entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                      Whitehead S., Barrell B.G.;
"The genome sequence of the food-borne pathogen reveals hypervariable sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      greA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-1995)
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[1]
                                                                                                                                                                                                               -!- FUNCTION: Necessary
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter jejuni.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                          GREA OR CJ0287C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9PIK9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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WormPep; ZK177.1; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol
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                                                                                                                                                                                                                                                                                                                                                                                                  Campylobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson K.
                                                                                                      SIMILARITY: BELONGS TO THE GREA/GREB FAMILY.
                                                                                                                               elongating RNA polymerases that pass through, resulting in locked ternary complexes. Cleavage of the nascent transcript by cleavage factors such as greA or greB allows the resumption of elongation from the new 3'terminus. GreA releases sequences of 2 to 3
                                                                                                                                                                   elongation past template-encoded arresting sites. The arrestin sites in DNA have the property of trapping a certain fraction elongating RNA polymerases that pass through, resulting in loc
                                                                                                                                                                                                               FUNCTION: Necessary for efficient RNA polymerase transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAMJE
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(Rel. 41, Last sequence update)
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(Rel. 41, Last annotation grea (Trans
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                                                                                                                                                                                                                                                                                                                                                                                                teria; Epsilonproteobacteria;
Campylobacter.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Transcript
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 460;
                                                                                                                                                                                                                                                     Campylobacter jejuni
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Best Local S
Matches 5
                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                   Pfam; PP00047; ig; 1.

SMART; SM00406; IGv; 1.

SMART; SM00406; IG LIKE; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Bence-Jones protein.

1 97 IG-LIKE.
                                                                                                                                                                                   DOMAIN
NON TER
SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seque
15-SEP-2003 (Rel. 42, Last annot
Ig lambda chain V-V region DEL.
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PROSITE; PS00830; GREAB 2; 1.

PROSITE; PS00830; GREAB 2; 1.

Transcription regulation; DNA-binding; Coiled coil; Complete COILED COIL (POTENTIAL).

DOMAIN 43 74 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A new subgroup of human L-chains of the structure of Bence-Jones protein DEL."; Eur. J. Biochem. 50:49-69(1974).
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PIR; E81447; E81447.
HSSP; P21346; IGRJ.
                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01985; L5HUDL.
HSSP; P80748; 2LOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
-!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- MISCELLANEOUS: THIS IS THE FIRST SEQUENCED V CHAIN SUBGROUP V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eulitz M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=75112179; PubMed=4452363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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48
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5; Conserv
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                                            EDNORPS 7
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EDNDRPA 54
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                                                                                                                                                                                        108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 01, Creaceu, (Rel. 01, Last sequence update) (Rel. 42, Last annotation update)
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                                                                                           Conservative
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                                                                                                                                                                                   11342 MW; B8E8ED9C09C9E451 CRC64;
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71.4%;
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71.4%;
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                                                                                                              Score 30;
Pred. No.
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Pred. No. 8.4;
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YIE2 HSVB4
ID YIE2 HSVB4
AC Q02484;
DT 01-CCT-1994
DT 01-CCT-1994
DT 16-CCT-2001
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YLII ECOLI STANDARD; PRT; 3
ID YLII ECOLI STANDARD; PRT; 3
AC P75804; Q9R7R6;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence up
DT 16-OCT-2001 (Rel. 40, Last annotation
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Best Local S
Matches 5
STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
Oshima T., Aiba H., Baba T., Fuji
                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIRS / MG1655;
STRAIRS / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a c
between the Swiss Institute of Bioinformatics and the EMBL
the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of a bovine herpesvirus 4 immediate-early RNA encoding a homolog of the Epstein-Barr virus R transactivator."; J. Virol. 67:773-784(195).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last amoutation update)
Hypothetical protein in IE2 5'region (Fragment).
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MEDLINE=93124571; PubMed=8380465;
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Gammaherpesvirinae.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
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                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                           "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli
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83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                         Fujita
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Pred. No. 32;
                                                                                                                                                                                       of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E0B6FAF287CC5315 CRC64;
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                         K., Hayashi K., Honjo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 AA.
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RESULT 13
ETV4_HUMAN
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Best Local :
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MEDLINE-93181246; PubMed-8441666;
Higashino F., Yoshida K., Fujinaga K., Kamio K., Fujinaga "Isolation of a cDNA encoding the adenovirus BIA enhancer protein: a new human member of the ets oncogene family.";
Nucleic Acids Res. 21:547-553(1993).
-!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR THAT BINDS TO THE THE ADENOVIRUS EIA GENE; THE CORE-BINDING SEQUENCE IS 5'[AC]GGA[AT]GT-3'.
-!- SUBCELUULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDINE-95293380; PubMed=7774926;

Mriedman L.S., Ostermeyer E.A., Lynch

Anderson L.A., Dowd P., Lee M.K., Rowe

Boyd J., King M.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Signal; Complete proteome.

SIGNAL 1 20 POTENTIAL.

CHAIN 21 371 HYPOTHETICAL PROTEIN YLII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 3:137-155(1996).
-!- SIMILARITY: STRONG, TO SYNECHOCYSTIS PCC 6803 SIA.CALCOACETICUS GLUCOSE DEHYDROGENASE-B (GDHB).
                                                                                                                                                                                                                                                                                                      "22 genes from chromosome 17q21: cloning, sequencing, characterization of mutations in breast cancer familia Genomics 25:256-263(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variant 4) (F1
ETV4 OR E1AF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 36, Last sequence update)
15-UTL-1998 (Rel. 36, Last annotation update)
Adenovirus ElA enhancer binding protein (ElA-F) (ETS translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                          SEQUENCE OF 90-551 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; E64821; E64821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE000186; AAC73924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D90721; BAA35532.1;
D90722; BAA35540.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENNORPT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDNORPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EG13480; yliI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41054 MW;
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71.4%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kajihara M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99DB08FA302F50B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        ynch E.D., Szabo C.I., Rowell S.E., Ellison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 371;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
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                                                                                                                                                                                                                                                                                                                                     and tumors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                    Meza
                                                                                                                                                                               K.;
                                                                                                         ENHANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00345; ETS DOMAIN 1; 1.
PROSITE; PS00346; ETS DOMAIN 2; 1.
PROSITE; PS00346; ETS DOMAIN 3; 1.
DNA-binding; Nuclear protein; Actival NON TER 1 ASP/GLUDOMAIN 116 142 ASP/GLUDOMAIN 215 311 GLN-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U18018; AAA95991.1
EMBL; D12765; BAA02234.1
HSSP; P28324; 1BC8.
TRANSFAC; T00885; -.
Genew; HGNC:3493; ETV4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P28322;
01-DEC-1992
01-DEC-1992
15-SEP-2003
                       Ets oncogene family that is differentially expressed is embryonic cells.";

Genes Dev. 6:481-496(1992).

-I- FUNCTION: BINDS TO THE PEAS MOTIF (5'-AGGAAG-3').

REGULATORY ROLE DURING EMBRYOGENESIS.

-I- SUBCELLULAR LOCATION: Nuclear.

-I- TISSUE SPECIFICITY: BEPDIDDYNIS AND THE BRAIN.

-I- PIN: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
ETV4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00178; Ets; 1.
Pfam; PF04621; ETS PEAS N; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000418; Ets.
InterPro; IPR006715; ETS PEA3_N.
InterPro; IPR002341; HSF_ETS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew, HGNC:3493, ETV4.

MIM, 600711; -.

GO; GO:0005634; C:nucleus; NAS.

GO; GO:0016563; F:transcriptional activator activity; NAS.

GO; GO:0006355; P:regulation of transcription, DNA-dependent; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                            MEDLINE=92192459; PubMed=1547944;
Xin J.-H., Cowie A., Lachance P., Hassel
"Molecular cloning and characterization"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETV4 OR PEA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     variant 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               501 DNQRPA
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5; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 42, Last annotation update)
s enhancer activator 3 (PEA3 protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
215
408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OR PEA-3. (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506
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BELONGS TO
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311
488
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.9%;
83.3%;
THE
                                                                                                                                                                                                                                                        acterization of PEA3, a new member of the differentially expressed in mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
Pred.
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GLN-RICH.
ETS-DOMAIN.
GNGS -> EMSD (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Activator; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9D649C8A1FBBD8DB
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                                                                                                                                                                                                                                                                                                                           Hassell J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ETS translocation
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- outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Mon

a collaboration -

outstation

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FUNCTION: PLAYS A ROLE IN T CELL PROLIFERATION AND
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Query Match

78.9%;

Score 30;

DB 1;

Length 620;

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RESULT 15
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                     01-OCT 1994 (Rel. 30, Created)
01-OCT 1994 (Rel. 30, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase ITK/TSK (EC 2.7.1.112)
kinase) (Tyrosine-protein kinase Lyk) (Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                Gibson S., Leung B., Squir
Hogg D., Mills G.B.;
"Identification, cloning,
T-cell-specific tyrosine l
                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=9127936; PubMed=8504851;

Tanaka N., Asao H., Ohtani K., Nakamura M., Sugamura K.;

"A novel human tyrosine kinase gene inducible in T cells by interleukin 2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00178; Ets; 1.
Pfam; PF04621; ETS PEA3 N; 1.
PRINTS; PR00454; ETSDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00345; ETS DOMAIN 1; 1.
PROSITE; PS00346; ETS DOMAIN 2; 1.
PROSITE; PS50061; ETS DOMAIN 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00454; ETSDOM SMART; SM00413; ETS; 1.
             on chromosome 5q.";
Blood 82:1561-1572(1993)
                                                           MEDLINE=93372354; PubMed=8364206; Gibson S., Leung B., Squire J.A., Hogg D., Mills G.B.;
                                                                                                                                       FEBS
                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                             Kinase) (Tyrosine-protein ITK OR LYK OR EMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P28324; 1BC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X63190; CAA44872.1;
                                                                                               TISSUE=Thymus;
                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000418; Ets.
InterPro; IPR006715; ETS_PEA3_N.
InterPro; IPR002341; HSF_ETS.
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                                                                                                                                                                                                                        CBI_TaxID=9606;
                                                                                                                                                                                                                                                                 lomo sapiens
                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MGI:99423; Etv4.
GO:0008045; P:motor axon guidance; IMP.
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315
492
60846
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Primates;
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83.3%;
                                   , and characterization kinase located at the
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GLN-RICH.
ETS-DOMAIN.
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Pred. No.
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                                                                                                                                                                                                                                       Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                      Hill M.,
                                                                                                                                                                                                                                                                                                                                                                   620 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
56;
                                                                                                                                                                                                                                                  Vertebrata; Euteleostomi;
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                                                                      Arima N.,
                                                                                                                                                                                                                                                                                          EMT)
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                                of a novel human hematopoietin complex
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                                                                        Goss P.,
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MIM; 186973; -.
GO:0004715; F:non-membrane spanni
GO; GO:0004715; F:non-membrane spanni
GO: GO:0006968; P:cellular defense re
InterPro; IPR001562; BTK.
InterPro; IPR001562; BTK.
InterPro; IPR001649; PH.
InterPro; IPR000719; Prot_kinase.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                           SMART; SM00107; BTK; 1.

SMART; SM00223; SH2; 1.

SMART; SM00223; SH2; 1.

SMART; SM00226; SH3; 1.

SMART; SM00326; SH3; 1.

SMART; SM00219; TyrKc; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00101; PROTEIN KINASE TYR; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS50001; SH2; 1.

PROSITE; PS50003; SH3; 1.

PROSITE; PS50003; PH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00402; TECBTKDOMAIN.
PRINTS; PR00109; TYKKINASE.
PRODOm; PD000001; PROLAINASE.
PRODOm; PD000001; PROLAINASE; 1
PRODOm; PD0000066; SH3; 1.
NP_BIND
BINDING
ACT_SITE
MOD_RES
CONFLICT
SEQUENCE
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HSSP; Q03526; 1AWJ.
Genew; HGNC:6171; ITK.
                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D13720; BAA02873.1; -.
EMBL; L10717; AAA36748.1; -.
EMBL; S65186; AAB28072.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no water by non-profit institutions as long as its content.
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Pfam; PF00169; PH; 1.
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                                                                                         DOMAIN
                                                                                                                                      DOMAIN
                                                                                                                                                      ATP-bi
                                                                                                                                                                  [ransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - TISSUE SPECIFICITY: T-CELL LINES AND
- INDUCTION: By interleukin-2.
- SIMILARITY: BELONGS TO THE TYR FAMIL
SUBFAMILY:
- SIMILARITY: Contains 1 SH2 domain.
- SIMILARITY: Contains 1 SH3 domain.
- SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIFFERENTIATION.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

SUBCELLULAR LOCATION: LOCALIZES TO CELL SURFACE RECEPTORS IN THE SUBCELLULAR ACCAPTION: ENGLISHED WITH RESPECTIVE RECEPTORS (TCR, CD28, CD2) IN T-CELLS (BY SIMULATION WITH RESPECTIVE RECEPTORS (TCR, CD28, CD2) IN T-CELLS (BY SIMULARITY).

TISSUE SPECIFICITY: T-CELL LINES AND NATURAL KILLER CELL LINES.
                                                                                                                                                  inding;
                                              171
171
239
363
369
391
482
                                                                                                                                                    SH2
                                                                                                                                                                Tyrosine-protein
                                                                                                                                                    domain;
      71831
                                                                                                                                                                                                                                                                                                                                                                              kinase;
                                                                                                                                                    SH3
    ¥
..
                                              PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
   PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
V -> W (IN REF. 2; AAB28072).
DAE396BD2309319D CRC64;
                                                                                                                                                  domain.
                                                                                                                                                                  kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spanning protein tyrosine kina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response;
                                                                                                                                                                  Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
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Search completed: January 12, 2004, 06:59:45 Job time : 5.82812 secs	Qy 1 EDNQRP 6    :   Db 162 EDNRRP 167	Best Local Similarity 83.3%; Pred. No. 64; Matches 5; Conservative 1; Mismatches
		0;
		0; Indels
		0;
		0; Gaps
		0;

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd

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Minimum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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sp_plant:*
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q8WW1B
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Q96JD2
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Q93D14
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Q82752
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Q96jdl homo sapien
Q96jd0 homo sapien
Q8ww18 homo sapien
Q49849 mycobacteri
Q80896 arabidopsis
Q96jd2 homo sapien
Q93d14 acinetobact
Q43955 leishmania
Q09534 caenorhabdi
Q82722 salmonella
Q8zpf2 salmonella
Q8zpf2 scalmonella
Q8cq75 oceanobacil
Q90x42 brachydanio
Q8tbc9 homo sapien
Q8dv81 streptococc
Q8g873 bifidobacte
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	Q.		Q9k394 vibrio chol	vibrio o	Q99cz2 bovine herp		Q9sjf6 arabidopsis		5 arabi		Q9fzr6 mycoplasma	Q8cw87 escherichia	Q8x6u6 escherichia	Q9rgr0 neisseria m	lymantria	Q9f3f6 streptomyce		brachy	O22922 arabidopsis		Q96iu0 homo sapien	Q8ghn3 pseudomonas			Q8exi6 leptospira	Q919b7 chlamydia t	Q9v4c9 drosophila	Q8vqv1 rhodococcus

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Mammalia; Eutheria; I
NCBI TaxID=9606;
[1]
  01-NOV-1996
01-NOV-1996
01-DEC-2001
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Q49849;
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"Amyloid lambda 6 light chain variable region SAR.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF267875; AAK58587.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig-WHC.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Similar to RIKEN cDNA 1700020L24 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Amyloid lambda 6 light chain variable region SAR (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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BC021727; AAH21727.1; -.
NCE 248 AA; 27236 MW; A988860B81AA530D CRC64;
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116 AA;
  (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                                         PRELIMINARY;
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12294 MW; F7B0E9F49FAE369E CRC64;
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Pred. No.
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Pred. No. (
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O1-NOV-1998
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Robiso
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
thallana.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
At232590 protein.
                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC004681; AAC25941.1; -. SEQUENCE 704 AA; 79017 MW; 69C8E8FD56C040FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AT2G32590.

Arabid3590 thaliana (Mouse-ear cress).

Arabid45; Viridiplantae; Streptophyta; Embryophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core el

Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.
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Mycobacterium leprae.
Mycobacteria; Actinobacteridae; Actinomycetales;
Bacteria; Actinobacteria; Mycobacterium.
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eurosids II; Brassicales;
NCBI_TaxID=3702;
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edons; core eudicots; Rosidae;
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RESULT 6 Q96JD2 ID Q96JD2

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Q93DLT 093D
AC Q93D
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Q93D14;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
O-methyltransferase-like protein.
                                                                                                       InterPro; IPR002935; Methyltransf_3.
InterPro; IPR000051; SAM bind.
Pfam; PF01596; Methyltransf_3; 1.
Methyltransferase; Transferase.
SEQUENCE 222 AA; 24730 MW; E8C02
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NON_TER
SEQUENCE
                                                                                                                                                                                 MEDLINE=21555098; PubMed=11698371;
Young D.M., Ornston L.N.;
"Functions of the Mismatch Repair Gene mutS from Acinetobacter sp.
Strain ADP1.";
J. Bacteriol. 183:6822-6831(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Bone marrow;
Perfetti V., Casarini S., Colli Vignarelli M.,
"Amyloid lambda 6 light chain variable region N
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ c
EMBL, AF267873; AAK58585 1; -.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Amyloid lambda 6 light chain variable region NEG (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleos
                                                                                                                                                                           EMBL; AF400582; AAK92498.1;
                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                             STRAIN=ADP1
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=62977;
                                                                                                                                                                                                                                                                                                                                          Acinetobacter sp. ADP1
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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 177
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; SM00406; IGv; 1.
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DNQRPS 182
                        DNQRPS 7
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85.7%;
                                                              86.8%; Score 33; 100.0%; Pred. No.
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                                                                                                        E8C020F41AD3CF67 CRC64;
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InterPro; IPR007007; Znf C2H2.
Pfam; PP00096; Zf-C2H2; 3.
SMART; SM00225; BTB; 1.
SMART; SM00225; BTB; 1.
PROSITE; PS00097; BTB; 1.
PROSITE; PS00097; BTB; 1.
PROSITE; PS00028; ZINC FINGER C2H2_1; 1.
PROSITE; PS00028; ZINC; ZÎNC-fÎNGET.
SEQUENCE 471 AA; 51751 MW; C9F780E3AEA;
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01-JAN-1999
01-MAR-2003
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O43955;
O1-JUN-1998
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Q09534;
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Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a transcription factor like locus in Leishmania mexicana amazonensis."; Mol. Biochem. Parasitol. 90:505-511(1997). EMBL; AF016581; AAC38851.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998
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                                                                                                                                                                                                                                                                                                                                       EMBL; Z48334; CAA88310.1;
                                                                                                                                                                                                                                                                                                                                                       investigating biology.";
Science 282:2012-2018(1998).
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                                                                                                                                                                                                                                                                                                                    NormPep; F10B5.3; CE01545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
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Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                                                                                  Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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9 (TrEMBLrel.
3 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9851916;
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cive 0; Mismatches
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09, Last sequence update)
23, Last annotation updat
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Pred. No. 80;
0; Mismatches
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative glycogen debranching protein (EC 3.2.1.-).
STY1505 OR STY4273.
Salmonella typhi.
                                      SEQUENCE FROM N.A.

STRAIN-LT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; PubMed-11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., N

Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nh

Materston R., Wilson R.K.;
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Nature 413:848-852(2001).
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STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
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InterPro; IPR002048; EF-hand.
InterPro; IPR004193; Glyco_hydro_13N.
Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase N; 1.
PROSITE; PS00018; EF_HAND; 1.
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"Complete LT2.";
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                                                                                                                                                                                                                                                                                                                            Salmonella typhimurium
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                                                                                                                                                                                                                                                 NCBI_TaxID=602;
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                   genome
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85.7%;
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                        of Salmonella
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Last annotation update)
(EC 3.2.1.-).
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Pred. No. 1e+02;
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N., Mulvaney E.,
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                        Typhimurium
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Q90X42;
O1-DEC-2001 (TrEMBLrel
O1-DEC-2001 (TrEMBLrel
O1-DEC-2002 (TrEMBLrel
O1-CT-2002 (TrEMBLrel
SC:dZ150F13.1 (Novel p
SC:DZ150F13.1.
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Q8EQ75;
01-MAR-2003
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InterPro;
InterPro;
         Corby N.;
Submitted
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STRALN=HTE831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., Uchiyama I.;
"Genome sequence of Oceanobacillus iheyensis is
Ridge and its unexpected adaptive capabilities
                                                                                                                                                                                                                                                                                                                                                                                                                                                       081838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00128; alpha-amylase; 1.
Pfam; PF02922; isoamylase N; 1.
PROSITE; P800018; EFF_HAND; 1.
Hydrolase; Glycosidase; Hypothetical protein; Cc
SEQUENCE 691 AA; 78569 MW; 318863462FBA6531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                          Bukaryota; Metazoa; Chordata;
Actinopterygii; Neopterygii; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003
01-MAR-2003
                   SEQUENCE FROM N.A. Corby N.;
                                             Cyprinidae; Dani
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                           environments."
                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=182710;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Oceanobacillus
                                                                                          Brachydanio rerio (Zebrafish)
                                                                                                                                                                                                                                                                                                           Complete proteome.
                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e 413:852-856(2001).
AE008768; AAL20476.1; -.
AE008047; Alpha amyl_cat.
Pro; IPR002048; EF-hand.
Pro; IPR004193; Glyco_hydro_13N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154 EDRORPS
tted (OCT-2001) to the AL591213; CAD10077.1;
                                                                                                                                                                                                                                                                                                                       AP004599;
                                                                                                                                                                                                                   49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EDNORPS
                                                                                                                                                                                                                                     1 EDNORPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                         Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                   EDNGRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Firmicutes;
                                                                                                                       (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                   193 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TIEMBLrel. 23, Created)
(TIEMBLrel. 23, Last sequence update)
(TIEMBLrel. 23, Last annotation update)
for IS660 (divided with OB1837 and OB1838).
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               iheyensis.
                                                                                                                                                                                                                                                                                                                       BAC13794.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       160
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                                                                                                                                                                                                                                                                                                                                30:3927-3935 (2002) .
                                                                                                                                                                                                                                                                                                   23201 MW;
                                                                                                                                                                                                                                                                     81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.2%;
85.7%;
                                                                                                            protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacillales;
                                                                                                                       Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                           0
                                                                                                                                             Created)
          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
                                                                      ; Craniata;
Teleostei;
                                                                                                              (Fragment).
                                                                                          (Danio rerio).
                                                                                                                                                                                                                                                                                                    6CFA619F8DAEB61C
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Oceanobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
No.
                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193
                                                                                                                                                                  221
                                                                                                                                                                                                                                                                       51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
1.2e+02;
                                                                                                                                                                                                                                                                                В
                                                                       Ostariophysi; Cypriniformes;
                                                                                 Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                16;
                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                 isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
31 CRC64;
                                                                                                                                                                                                                                                                                                                                                      ç
                                                                                                                                                                                                                                                                                Length 193;
                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                      extreme
                                                                                Euteleostom1;
                                                                                                                                                                                                                                                           0
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SQ

NON TER SEQUENCE

221 AA;

1 25208 MW;

F0B3D4CAD91CACE1 CRC64;

Query Match Best Local S Matches 5

Local Similarity les 5; Conserv

Conservative

2; Mismatches Score 31; Pred. No. 5

81.6%;

DB 13; Length 221; 59; 0;

Indels

<u>.</u>

Gaps

0

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RESULT 14
Q8TBC
D8TBC
AC Q8TBC
DT 01-VI
DT 01-W
DT 01-
       문
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Best Local Similarity
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01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUB-B-Cell;

Strausberg R.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; BC022823; AAH22823.1; -.

InterPro; IPR003006; Ig_wHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 2.

SMART; SM00406; IGv; 1.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative 1-acylglycerol-3-phosphate O-acyltransferase
2.3.1.51).
                                                                                     SEQUENCE FROM N.A.

STRAIN-UAN159 / ATCC 700610 / Serotype C;

MEDLINE=22295063; PubMed=12397186;

Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,

Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,

Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti

"Genome sequence of Streptococcus mutans UA159, a cariogenic d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8DV81;
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. SEQUENCE 233 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TBC9;
pathogen.";
Proc. Natl. Acad. Sci. U.S.A.
EMBL; AE014906; AANS8358.1; -.
Acyltransferase; Transferase;
                                                                                                                                                                                                                                                                                                                                                  Streptococcus mutans.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                       NCBI_TaxID=1309;
[1]
                                                                                                                                                                                                                                                                                                                                     Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                     SMU.624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8DV81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141
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•-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (TrEMBLrel.
2 (TrEMBLrel.
3 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24867 MW; 367411BFD6F4DF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21,
21,
23,
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 31;
Pred. No.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                  99:14434-14439(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            233 AA
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J.J.;
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                S
                                                                       QS
                                 Query Match
Best Local Similarity
Matches 5; Conserv
                                                                        SEQUENCE
201
         1 EDNQRPS 7
KDNERPS 207
                                                                        250 AA;
                                    Conservative
                                                                        29051 MW;
                                           81.6%;
                                  Score 31; DB:
Pred. No. 68;
2; Mismatches
                                    <u>ب</u>
                                                                        412A631E431A2C3B CRC64;
                                                     DB 16; Length 250;
                                    <u>.</u>
                                    Indels
                                    0
                                  Gaps
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0

Search completed: January 12, 2004, 07:02:13 Job time : 19.2188 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A_Geneseq_19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
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38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1107863 seqs, 158726573 residues
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                                                             SID51/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

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Copyright (c) 1993 - 2004 Compugen Ltd.
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

9	œ	7	6	5	4	w	N	ᆫ	Result No.
34	34	34	38	38	38	38	38	38	Score
89.5	89.5	89.5	100.0	100.0	100.0	100.0	100.0		Query Match 1
106	101	7	258	161	113	98	7		% Query Match Length DB
15	22	18	23	22	22	24	24	22	DB.
AAR54054	ABB12331	AAW16592	ABP45223	AAG76011	AAU02522	ABP56510	ABU11263	AAB61297	IJ
Sequence of the VL	Human bone marrow	Anti-RSV F glycopr	Human BLyS binding	Human colon cancer	Anti-adipocyte mon	Human anti-Fc-epsi	Human TANGO 268 VL	Anti-TANGO 268 scF	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	Ω 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
30	31	31	31	31	31	31	31	31	31	31	31	31	31	ω [΄] 11	32	32	32	32	33	33	u u	33	33	33	ω ω	33	33	34	34	34	34	34	34	34	34
78.9	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	81.6	84.2	84.2	84.2	84.2	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	86.8	89.5	89.5	89.5	89.5	89.5	89.5	89.5	89.5
- 7	738	395	253	250	248	248	235	235	123	108	108	108	95	7	245	108	108	108	259	253	252	248	114	114	112	110	88	246	244	233	114	109	109	106	106
22	22	23	23	23	23	23	24	24	22	21	21	17	23	23	23	18	17	15	23	23	23	23	24	24	18	23	22	22	23	23	21	18	18	18	17
AAU08352	ABB58805	ABP65262	ABP45477	ABP45529	ABP45963	ABP45954	АВJ19837	ABJ19836	AAM24233	AAY68900	AAY68898	AAR88719	ABP02892	AAU70344	ABP45703	AAW24988	AAW01523	AAR54051	ABP45266	ABP45216	ABP45117	ABP45262	ABP56512	ABP56511	AAW08488	AA018434	AAU56093	ABB12413	ABP45831	AAU82012	AAB53654	AAW14785	AAW16588	AAW24991	AAW01529
Antibody light cha	Drosophila melanog	Bifidobacterium lo	BLyS			BLyS	٠	Human VEGF-2 relat	Human EST encoded	Variable region of	The variable regio	Human antibody lam	Human ORFX protein	Human lambda III l	Human BLyS binding	Monoclonal antibod	Monoclonal antibod	щ						Human anti-Fc-epsi	C6 human sFv antib	Anti-GD2 antibody	Propionibacterium	Human bone marrow	Human BLyS binding	Human secreted pro	Human colon cancer	ò	•	Monoclonal antibod	Monoclonal antibod

### ALIGNMENTS

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30-JUN-1999; 99US-0345468. 06-DEC-1999; 99US-0454824. 14-PEB-2000; 2000US-0503387. (MILL-) MILLENNIUM PHARM INC.	04-JAN-2001. 30-JUN-2000; 2000WO-US18152.	HOMO Bapiens WO200100810-A1.	blood vessel injury, thrombotic disorder, haemorrhagic disorder, stroke; ischaemia; cardiovascular disease; immunological disease; liver disorder; cancer.	Human; antibody; scFv; CDR; complementarity determining region; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder;	Anti-TANGO 268 scFv CDR, SEQ ID NO: 65.	AAB61297; 04-APR-2001 (first entry)	RESULT 1 AAB61297 AAB61297 standard; Peptide; 7 AA.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboembolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; cardiovascular disease; angina pectoris; myocardial infarction; coronary restenosis; atherosclerosis; immunological disorder; developmental disorder; embryonic disorder; liver disorder; cerebral vascular disease; venous thromboembolism disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity (GPVI. These disorders include bleeding disorders (e.g. thrombotyticopaenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardienfarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent acture especially of the colon and liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Busfield SJ, Viller Oian MD, Kingsbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, tr and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                       09-APR-2001; 2001US-0829495.
                                                                                                                                                                                                                                   09-APR-2002; 2002WO-US11122
                                                                                                                                                                                                                                                                                                                                                                                                                           WO200280968-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                (MILL-) MILLENNIUM PHARM INC
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ngsbury G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 9.3e+05;
Mismatches 0;
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RESULT 3 ABP56510

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> 1 EDNORPS 7 Similarity 7; Conser

Conservative

100.0%;

.0%; Score 38; DB 24, 0.0%; Pred. No. 9.3e+05;

Length 7; Indels

<u>,</u>

Gaps

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EDNORPS

Query Match Best Local S Matches 7

Sequence

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WO200282085-A2 Synthetic Homo sapiens 20-MAR-2003

(first

entry)

ABP56510;

ABP56510 standard;

Protein;

Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive; allergic disease; urticaria; late phase allergic reaction; malignanc intrinsic asthma; drug intolerance; food intolerance; immunoglobulin conditional autoimmunity; IgE mediated disease.

:ion; malignancy;
immunoglobulin E;

Human anti-Fc-epsilon-R1 alpha autoantibody light chain V1-22

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CC of which specifically binding to a TANGO 268 (also referred as glycoprotein CC vi (GPVI)) antigen. The antibodies of the invention act to decrease or CC block TANGO 268 binding to extracellular matrix components, or as a CC collagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration, CC morphology, differentiation and/or function of megakaryocytes and CC platelete, including during development e.g. embryogenesis, modulating platelete, including during development e.g. embryogenesis in cluding clarelete and platelet-endothelium interactions in CC inflammation and/or thrombosis, and modulating platelet aggregation and CC inflammation. They are also useful for modulating disorders associated CC with abnormal or aberrant megakaryocyte and/or platelet proliferation, comigration, morphology, differentiation and/or platelet proliferation, CC migration, morphology, differentiation and/or platelet proliferation, condulated by these antibodies are thrombotic disorders, cerebral CC vascular diseases (e.g. diseases including are thrombotic disorders, cerebral CC vascular diseases including angina pectoris, myocardial infarction, coronary CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular CC diseases including angina pectoris, myocardial infarction, coronary CC restencels, atterosclerosis, etc); immunological disorders, cerebral CC vascular diseases, venous thromboembolism diseases, coronary diseases a cc cand metastatic cancers. The antibodies of the invention only causes a cc methods. The present source represents a pestide sequence used to used to used to some advantages over prior art
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to a novel purified antibody comprising variable heavy (VH) complementarity determining region (CDR)1, or VH CDR3; or VH CDR3 and VL CDR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Busfield SJ, Villeval J, Qian DM, Kingsbury G;
                                               generate
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                                                                           The present sequence represents a peptide sequence used to
A
A
                                               antibodies of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VH CDR2
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RESULT 4
AAU02522
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain for identifying and obtaining an inhibitor of a pathological process; (2) use of the identified inhibitor for inhibiting activity of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and (3) a compound identified by the method, which binds but does not activate the receptor; and (4) a polypeptide capable of specific binding to the Fc-epsilon-R1 receptor (4) a polypeptide capable of specific binding to the Fc-epsilon-R1 receptor between obtaining an inhibitor of a pathological process e.g. imbalance between cell-bound and free IgE e.g. allergic disease (urticaria, late phase allergic reactions, intrinsic asthma, drug intolerance and food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying and obtaining inhibitor of a pathological process for treating e.g. autoimmunity comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor and an autoantibody against its alpha-chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allergic reactions, intrinsic asthma, drug intolerance and food intolerance), IgE mediated disease or malignancy. The compound is useful for treating a patthological process, particularly conditional autoimmunity. The present sequence represents a human recombinant anti-Fc-epsilon-Rl alpha autoantibody light chain protein sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a method for identifying and obtaining an inhibitor of a pathological process. The method comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-Rl receptor alpha-chain and an autoantibody against its alpha-chain. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 20;
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                                                                                                                                                                                                                                                                                                                                              AAU02522 standard; Protein; 113 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
              12-OCT-1999;
                                               11-OCT-2000; 2000WO-GB03900
                                                                                                                   WO200127279-A1
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                     heart disease;
                                                                                                                                                                                                                                       Anti-adipocyte monoclonal antibody light chain, FAT 13
                                                                                                                                                                                                                                                                           29-AUG-2001
                                                                                                                                                                                                                                                                                                            AAU02522;
                                                                                                                                                                                                     Antibody; adipocyte; heavy chain; light chain; obesity; fat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZLBB-) ZLB BIOPLASMA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                   51 EDNORPS 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EDNORPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                     complementarity determining region; CDR
              99US-0158812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24; Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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WPI; 2001-235357/24.
N-PSDB; AAH35416.
                                                                                                                                                                                                                                                                                                                      Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 22.
                                                                                                                                                                                                                                                                                                                                                                        Human colon cancer antigen protein SEQ ID NO:6775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 106; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAS03422
                                                  Ruben SM,
                                                                                                                        29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-2001 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG76011 standard; Protein; 161
                                                                                                                                                                          28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                 WO200122920-A2
                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                     (HUMA-) HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-282031/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EDNORPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDNORPS 59
                                                  Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                     GENOME SCI INC
                                                                                                                        99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
                                                     Birse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>,</u>
                                                    G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB Pred. No. 3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                    Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 6
ABP45223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, character with decreased expression. N and P may be used the treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing in a patient's genome that affect the patients own production of P. Additionally, N may be used to produce the colon cancer-associated P. Additionally, N may be used to produce the colon cancer-associated P. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB37789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 7
                                                                                                                    17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.

N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                     immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
WPI; 2002-114799/15
                                                                                                                                                                                                                                 10-JAN-2002.
                                                                                                                                                                                                                                                             WO200202641-A1
                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                     BLys; B lymphocyte stimulator; tumour necrosis factor; B cell
                                                                                                                                                                                                                                                                                                                                                                                                                               Human BLyS binding scFv SEQ ID 1234.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP45223;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP45223 standard; Protein; 258
                            Ruben SM,
                                                         (HUMA-)
                                                                                                                                                                 16-JUN-2000;
                                                                                                                                                                                                 15-JUN-2001; 2001WO-US19110.
                                                                                                       25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72
                                                         HUMAN GENOME
CAMBRIDGE ANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDNORPS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDNORPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                           Barash SC,
                                                                                                    ; 2000US-212210P.
; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                           ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                           SCI INC
                            Choi GH,
                                                         TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                     TNF superfamily; human; proliferation; B cell d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                           Vaughan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                            Hilbert D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                     n; cytostatic;
differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
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198 EDNORPS 204

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Best Local
                                         Matches
                                                                                                                                                                            cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TWF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 1874-1875; 3148pp; English
                                                                                                                        Sequence
                                                                                                                                                               of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
  1 EDNORPS 7
                                       . Similarity 7; Conserv
                                                                                                                        258 AA;
                                       Conservative
                                                            100.0%;
                                           0
                                         Score 38; DE
Pred. No. 8.5
0; Mismatches
                                                              DB .5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 j polypeptides, u
immune disorders
                                                                                23;
                                           0
                                                                              Length 258;
                                                                                                                                                                                                                                                                                                                                                                                                                              invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for
                                             0
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                      BLyS
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RESULT 7
AAW16592
                                                                                                                                                                                                                                                                                                                                                                Respiratory syncytial virus; RSV; monoclonal antibody; complementarity determining region; pneumonia; bronchic
                                                                                                                                                                                                                                              27-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                diagnosis; therapy; vaccine; RSVF2-5
                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-RSV F glycoprotein antibody RSVF2-5 light chain VL6 CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW16592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW16592 standard;
                   Composition
                                                     WPI; 1997-202621/18
                                                                                                                                                                            18-SEP-1995;
                                                                                                                                                                                                          18-SEP-1996;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                       Chanock RM,
                                                                                                                         (USSH)
                                                                                                                                          (INTR-)
                                                                                                                     INTRACEL CORP
US DEPT HEALTI
                                                                                                                          DEPT HEALTH & HUMAN SERVICES.
n comprising
                                                                                       Crowe JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                            95US-0003931.
                                                                                                                                                                                                              96WO-US14937.
rising respiratory syncytial virus antibody prophylaxis of active disease or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide; 7
                                                                                        Gilmour PS,
                                                                                                                                                                                                                                                                                                                                                                  region; pneumonia; bronchiolitis;
                                                                                       Murphy
                                                                                        BR,
                                                                                        Pilkington
                                                                                                                                                                                                                                                                                                                                                                                     CDR;
                                                                                          g;
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This peptide sequence comprises 2 (CDR2) of the light chain VL6

complementarity determining region region of a novel neutralising

Claim 8; Page 56; 71pp; English

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RESULT 8
ABB12331
ID ABB1
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The antibody, designated RSVP2-5 (ATCC 69909), selectively binds to an RSV F glycoprotein epitope. DNA encoding RSVP2-5 Fd and light chain (see AAT66556-57) was isolated from a phage library prepared from the RNA of peripheral blood lymphocytes of an HIV-1 infected conor. A claimed pharmaceutical preparation comprises a carrier and antibody that includes the RSVP2-5 VH3 CDR3 (AAW16586) and condition of the entire Fd region (AAW1580), or is an Fab fragment and includes the RSVP2-5 VH3 CDR3 (AAW16582) con the entire Fd region (AAW16580), or is an Fab fragment and includes the RSVP2-5 VH3 CDR3 (AAW16590) or entire CDR3 (AAW16594), CDR2 (CDR2, CDR1 (AAW16590)) or entire CDR3 (AAW16594), CDR2 (CDR2, CDR3 (AAW16590)) or entire CDR3 (AAW16594), CDR3 (AAW16590) or entire CDR3 (CAW16598). The preparation alternatively comprises a CC carrier and a vector that includes a nucleotide sequence encoding CC the antibody. The preparations can be used for the treatment or composition of active RSV disease or infection (claimed), and may composite the condition of the condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
23-AUG-2000; 2000US-0649267.
30-NOV-2000; 2000US-250583P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer; antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
                                                                                                                        New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, canculation of increasing hematopoiesis, stem cell survival and bone growth and
                                                                                                                                                                                                                                                                                                 WPI; 2001-626375/72.
N-PSDB; ABA09575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;
immunostimulant; analgesic; cerebroprotective; antianaemic; infe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human bone marrow expressed protein SEQ ID NO: 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB12331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB12331 standard; Protein; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         also be used for RSV detection. The antibody binds and antigenic subgroups A and B of RSV with high efficiency.
Claim 10; Page 200-201; 380pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-2001; 2001WO-US10472.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200174836-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nervous system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                              ΥŢ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDNQRP 6
                                                                                                                                                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                              쫩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                          Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 18;
9.3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                              Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                              뭔
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                                                                                                                        neurological, cancer and bone growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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The present invention relates to bone marrow expressed polynucleotides

Human volunteers were immunised with hepatitis B vaccine. 2, ZM1-1 and PE1-1 hybridoma cell lines were derived from

MD3-4,

ZM1-

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RESULT 9
AAR54054
ID AAR5
888888888888
                                                                                                                                                                                                                                                                                                                                                                      FF XXX XXX DD XXX XXX
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                                                                                                                                                                                                                                                                                                                                               FT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, centra and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a
                                                     Monoclonal antibodies active against Hepatitis B surface antigen - for diagnosis and treatment of Hepatitis B virus
                                                                                       WPI; 1994-183497/22.
N-PSDB; AAQ64057.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                        Ostberg
                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of hepatitis B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
08-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR54054 standard; Protein; 106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein of
                                Example; Page 43; 53pp; English
                                                                                                                                                                       06-NOV-1992;
                                                                                                                                                                                             06-NOV-1992;
                                                                                                                                                                                                                                          WO9411495-A1
                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus; surface antigen; monoclonal antibody; therapy; HBsAG; diagnosis; HBV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR54054;
                                                                                                                                               (SANO ) SANDOZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 EDNKRPS 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDNORPS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             the VL region of monoclonal antibody MD3-4 against
virus surgace antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                                                               LTD.
                                                                                                                                                                       92WO-US09749
                                                                                                                                                                                              92WO-US09749
                                                                                                                                                                                                                                                                                                          /label= CDR 1
50..56
/label= CDR 2
                                                                                                                                                                                                                                                                         /label= CDR 3
95..106
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                                                                                                                                                                                                                                                                /label= J 3
                                                                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.5%;
                                                                                                                                                                                                                                                                                                                                                          V III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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21;
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RESULT 10
AAW01529
ID AAW01
XX
AC AAW01
XX
DT 25-M
DT 25-M
DT 04-M
XX
DT 04-M
XX
MONG
KW MONG
KW Xen
YM
XX
FT Re
F
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Best Local S
Matches 6
21-APR-1992;
05-SEP-1986;
31-OCT-1986;
11-MAY-1988;
15-JUN-1990;
27-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lymphocytes of individuals immunised with Heptavax (Merck & CO). Antibodies PE1-1, ZM1-1, MZ1-2 and MD3-4 belong to the IgG1 clas. The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as ATCC HB9234, 9191 and 9192 respectively. The cell lines all behave as typical (mouse x human) x human hybridomas and produce their respective Abs in concs. ranging up to 25 mg/l in standard suspension culture. The heavy variable (VH) and light variable (LH) chains of Abs PE1-1, ZM1-1, ZM1-2 and MD3-4 were isolated and sequenced. Total RNA was extracted from 10(7) hybridoma cells of each cell line. ss DNA was synthesised using AMT-reverse transcriptase and oligo-dT as primer. PCRs were performed and amplified DNA was size selected. ss DNA for sequencing was isolated from each positive clone after superinfection with M13K07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; diagnosis; treatment; infection; hepatitis B; xenogeneic hybridoma; SPAZ 4; PE1-1; ZM1-1; ZM1-2; MD3-4; L03-3; IgG1 class; heavy chain; light chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-2003
04-MAR-1997
                                                                                                                                                                                   14-JUN-1994;
                                                                                                                                                                                                                                    15-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Monoclonal
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                                                                                                                                                                                                                                                                                       US5565354-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on 25-MAR-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody MD3-4 light chain variable region
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(first en
88US-0192754.
90US-0538796.
91US-0676036.
                                                                           92US-0871426.
86US-0904517.
86US-0925196.
                                                                                                                                                                                      94US-0259372
                                                                                                                                                                                                                                                                                                                               95..106
/label= J_kappa_3_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= framework_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= V_kappa_III_region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l= framework_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB
Pred. No. 22;
1; Mismatches
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AAW24991
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Best Local S
Matches 6
                                                                                                                                                                                                                                                       Heavy chain; light chain; variable region; human; monoclonal antibody; immunisation; hepatitis B virus; HBV; vaccine; mouse; fusion; xenogene; peripheral blood lymphocyte; surface antigen; cell culture; ion exchan; chromatography; size separation; primer; PCR; polymerase chain reaction amplification; hybridoma; infection; immunosuppression; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibodies effective for the diagnosis and treatment of diseases caused by infection with hepatitis B have been prepared fro cell line obtained by fusing a senogenetic hybridoma designated SPAZ with blood cells of a patient immunised with hepatitis B vaccine. Specific antibodies are PEI-1, ZMI-1, ZMI-2, MD3-4 and LO3-3, each c these being of the IgG1 class. The present sequence is the light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-476304/47
N-PSDB; AAT46135.
                                                                                                                                                                                                                                                                                                                                               25-MAR-2003
08-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  these being of the IgG1 class. variable chain of MD3-4.
                   06-JUN-1995;
                                                                                                Region
                                                                                                                     Domain
                                                                                                                                                                                                   Key
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                         Monoclonal antibody MD3-4 V1 region
                                                                                                                                                                                                                                                                                                                                                                                                      AAW24991 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                             Domain
                                                                                                                                                                   Domain
                                                                                                                                                                                       Region
                                                                 US5648077-A.
                                                                                                                                                                                                                                                liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              man monoclonal antibodies specific for hepatitis B surface antigen are used to treat or prevent infection or in diagnostic assays
                                                                                                                                                                                                                                             transplant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 EDNKRPS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 EDNORPS 7
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(first entry)
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                    95US-0468671
                                                                                                                                            /note=
                                                                                                                                                                  /note= "VlIII region"
24..33
                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                /note=
                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                       Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.5%;
                                                                                       "Jl3 region
                                                                                                           "complementarity
                                                                                                                                "complementarity
                                                                                                                                                      "complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
22;
                                                                                                                                  determining
                                                                                                                                                        determining
                                                                                                             determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                             region
                                                                                                                                   region
                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L03-3, each of
                                                                                                                                                                                                                                                                        chain reaction;
                                                                                                                                                                                                                                                                                n; xenogeneic;ion exchange;
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d from a
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21-APR-1992;

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RESULT 12
AAW16588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC from the human monoclonal antibody (MAD) MD3-4. The MAD was generated by immunising humans with a hepatitis B virus (HBV) vaccine, isolating peripheral blood lymphocytes (PBL) and fusing them with a mouse/human cc peripheral blood lymphocytes (PBL) and fusing them with a mouse/human cc zmnogeneic cell line SPAZ-4. 5 cell lines were isolated: PEI-1, ZMI-1, ZMI-2, MD3-4 and LO3-3. The cell lines were isolated: PEI-1, ZMI-1, C ZMI-2, MD3-4 and LO3-3. The cell lines were inclated: PEI-1, ZMI-1, C ZMI-2, MD3-4 and LO3-3. The cell culture by protein A cromatography, size separation on Sephacryl 3300 gel and ion exchange C chromatography on Q-Sepharose. The heavy and light chains of the MADs comparated and their amino acid sequences determined. Primers were generated and used to amplify CDNA synthesised from RNA purified from C generated and amino acid) from MADs PEI-1, ZMI-1, ZMI-2 and MD3-4 care shown in AAT85838-45 and AAW24984-91. The MADs can be used to treat LBV infections in immunosuppressed patients or patients with chronic active hepatitis, especially liver transplant patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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15-JUN-1990;
27-MAR-1991;
                                                                                                                                                   Respiratory syncytial virus; RSV; monoclonal antibody; CDR; complementarity determining region; pneumonia; bronchiolitis; diagnosis; therapy; vaccine; RSVF2-5.
                                                                                                                                                                                                                                                                                                   AAW16588 standard; Protein; 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Column 23-24; 25pp; English.
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                                                                                                                                                                                                            Anti-RSV F glycoprotein antibody RSVF2-5 light chain VL6.
                                                                                                                                                                                                                                          30-NOV-1997
                                                                                                                                                                                                                                                                     AAW16588;
                                         Region
                                                                                                                           Homo sapiens.
                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SANO ) SANDOZ
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                        EDNKRPS 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of hepatitis B - with human monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                          (first entry)
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86US-0925196.
88US-0192754.
90US-0538796.
91US-0676036.
94US-0259372.
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                          20..32
/label= CDR1
                                                                                             Location/Qualifiers
note= "framework region 1"
                                                                     /label= FR1
                                                                                                                                                                                                                                                                                                                                                                                                                                             89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB:
Pred. No. 22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Length 106;
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RESULT 13
AAW14785
ID AAW14
XX

AAW14785 standard; Protein; 109 AA

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                                                                                                                                                        of a novel neutralising human monoclonal antibody to respiratory constructions (RSV). The antibody to designated RSVP2-5 (ATCC 6909), selectively binds to an RSV F glycoprotein epitope. CDNA encoding the RSVF2-5 Fd VH3 and light chain VL6 (see AAT66556-57) was isolated from a phage library prepared from RNA extracted from the peripheral blood lymphocytes of an HIV-1 infected donor. A claimed pharmaceutical preparation comprises a carrier and an antibody that includes the RSVF2-5 VH3 CDR3 (AAW16586) and which may calso include the VH3 CDR2 (AAW16584) and/or CDR1 or the entire Fd region (AAW16588), or is an Fab fragment and further includes the RSVF2-5 VL6 CDR3 (AAW16594), CDR2 (AAW16594), CDR1 (AAW16590) or entire RSVF2-5 VL6 CDR3 (AAW16594), CDR2 (AAW16592), CDR1 (AAW16590) or entire carrier and a vector that includes a nucleotide sequence encoding the antibody. The preparations can be used for the treatment or prophylaxis of active RSV disease or infection (claimed), and may also be used for RSV detection. The antibody binds and neutralises can be used for RSV detection. The antibody binds and neutralises
                                                              Matches
                                                                              Query Match
Best Local
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 52-53; 71pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide sequence comprises the light chain VL6 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composition comprising respiratory syncytial virus antibody - useful for treatment or prophylaxis of active disease or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAT66557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-202621/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chanock RM, Crowe JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-SEP-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INTR-) INTRACEL CORP.
48
                             1 EDNORP 6
                                                              6
                                                                               Similarity
EDNORP 53
                                                                                                                                109 AA;
                                                              ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0003931.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33..47
/label= FR2
/note= "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= FR3
/note= "fra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= FR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= CDR2
                                                                              89.5%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "complementarity determining region (Claim 8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilmour PS, Murphy BR,
                                                              0,
                                                                Mismatches
                                                                                               DB 18; Length 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pilkington GR;
                                                                Indels
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                                                              Gaps
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AAW14785

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48

EDNORP 53

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Query Match
Best Local S
Matches 6
                                                                                           region (AAW14784) are provided of a novel, fully human monoclonal antibody (MAb), designated RSVF2-5, which selectively binds to the F glycoprotein of respiratory syncytial virus (RSV) and which neutralises RSV in vivo. To obtain RSVF2-5, a packaged phage library was prepd. from amplified heavy and light chain variable region clones derived from the peripheral blood lymphocytes of an HIV-1 infected donor. The phage library was panned with RSV proteins and isolated clones were sequenced. Isolated nucleic acids (AATG3417-18) can be used to produce novel polypeptides, esp. Fd or Fab fragments useful in the diagnosis of RSV disease, in methods for detecting the presence of RSV in a sample, and in the immunoprophylaxis and immunotherapy of RSV disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Respiratory syncytial virus; RSV; monoclonal antibody; Ndiagnosis; prophylaxis; immunotherapy; therapy; Fab; Fd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human monoclonal antibody RSVF2-5 light chain VL6
                                                                             Sequence
                                                                                                                                                                                                                                                          Claim 10; Page 49-50; 68pp; English
                                                                                                                                                                                                                                                                                  disease
                                                                                                                                                                                                                                                                                         Monoclonal ant for diagnosis
                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                         WPI; 1997-202886/18.
                                                                                                                                                                                                                                                                                                                                                              Gilmour PS,
                                                                                                                                                                                                                                                                                                                                                                                                          18-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               18-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9711177-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                    (INTR-) INTRACEL
                                Similarity 6; Conser
. EDNORP 6
                                                                                                                                                                                                                                                                                           antibody specific for respiratory syncytial virus sis and immuno-prophylaxis or immuno-therapy of RSV
                                                                             109 AA
                                                                                                                                                                                                                                                                                                                                                             Pilkington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= CDR3
/note= "Claim 7"
99..109
                                                                                                                                                                                                                                                                                                                                                                                                          95US-0003931
                                                                                                                                                                                                                                                                                                                                                                                                                                96WO-US14944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= CDR2
'note= "Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note= "Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= CDR1
                                           89.5%; Score 34;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L= FR2
                                                                                                                                                                                                                                                                                                                                                               GR
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                                   Mismatches
                                            DB 18;
. 23;
                                 °,
                                                     Length 109;
                                   Indels
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                                 Gaps
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RABSULT 14
AAB53654
ID AAB53
XX AAB53
XX AAB53
XX AAB53
XX AAB53
XX DF O9-MA
DE Human
XX Human
XX Human
XX ident
KW infect
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XW repr
XW repr
XX Infect
밁
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                                                                                                                              Matches
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                            neuroprotective, immunomodulatory, gynaecological, gastrointestinal, neuroprotective, immunomodulatory, gynaecological, gastrointestinal, vulnerary, nephrotropic, antiinfective and antibacterial activities, and can be used in gene therapy. The colon cancer antigen polynucleotides, proteins and antibodies to the proteins are useful for the prevention, treatment and diagnosis of colon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, such as for chromosome identification, and as hybridisation probes. The proteins may also be used to prevent diseases such as neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, wounds, renal disorders, infectious diseases, and cardiovascular disorders. AAC98764 to AAC98772 and AAB54007 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC97991 to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigens, given in AAB53234 to AAB54006. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon cancer associated gene sequences, referred to as colon cancer antigens, useful for the treatment, prevention, and diagnosis of colon
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 1776; 2104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders such as colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAC98411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-2000; 2000WO-US05883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunomodulatory; muscular; gynaecological; gastrointestinal;
nephrotropic; antiinfective; antibacterial; gene therapy; wound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; colon cancer; colon cancer antigen; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human colon cancer antigen protein sequence SEQ ID NO:1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB53654 standard; Protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human colon cancer antigens can have cytostatic, cardioactive, muscular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-587534/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200055351-A1.
                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infectious disease; cardiovascular disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dentification; cytostatic; cardioactive; neuroprotective;
                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA,
   37
                                                           1 EDNORPS 7
                                                                                                                           Similarity 6; Conserv
   EDNKRPS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ruben SM;
                                                                                                                                                                                                                                                            114
                                                                                                                           Conservative
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A
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                                                                                                                                                               89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the treatment,
                                                                                                                                                               Score 34;
Pred. No.
                                                                                                                                 Mismatches
                                                                                                                                                               DB
24;
                                                                                                                                                                                             21;
                                                                                                                              0
                                                                                                                                                                                          Length 114;
                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vulnerary;
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                                                                                                                                 Gaps
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RESULT 15

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Query Match
Best Local Similarity
Thes 6; Conserve
                                                                                                                         as SECP-1 to SECP-44) and the nucleic acids encoding them. Also cincluded are a host cell transformed with the nucleic acid, a transgenic animal comprising the nucleic acid, an anti-SECP antibody, use of the SECP proteins in isolating agonists and antagonists of SECP activity and a method of isolating compounds which alter the expression of the SECP pucleic acid. The SECP polynucleotides and prevention of cardiovascular (e.g. atherosclerosis, hypertension, myocardial cardiovascular (e.g. atherosclerosis, hypertension, myocardial cardiovascular (e.g. atherosclerosis, hypertension, myocardial confined (AIDS), altergies, rheumatoid arthritis), cell proliferative (e.g. cancer), developmental (e.g. Duchenne and Becker muscular (e.g. cancer), davelopmental (e.g. Duchenne and Becker muscular disorders. Numerous other examples of each disorder are given in the specification. The present sequence represents a SECP protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2000; 2000US-212890P.
23-JUN-2000; 2000US-213466P.
27-JUN-2000; 2000US-214601P.
31-JUL-2000; 2000US-222772P.
08-SEP-2000; 2000US-231435P.
15-SEP-2000; 2000US-232889P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppressive; antiviral; anti-HIV; antiarthritic; antirheumatic; muscular active general; anticonvulsant; noctropic; neuroprotective; antiallergic; hypotensive; cardiovascular disorder; atherosclerosis; hypertension; myocardial infarction; autoimmune disorder; inflammatory disorder; AIDS; acquired immunodeficiency syndrome; allergy; rheumatoid arthritis; cell proliferative disorder; cancer; developmental disorder; Duchenne muscular dystrophy; neurological disorder; epilepsy; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Forty four human secreted proteins (referred to as SECP-1 to SECP-44), useful in the diagnosis, treatment and prevention of cardiovascular (e.g. atherosclerosis), autoimmune/inflammatory (e.g. allergies) and cell proliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillman JL, Tang YT, Yue H, Elliott VS, Tribouley CM, Lee EA; Ramkumar J, Lal P, Xu Y, Warren BA, Hafalia AJA, Baughn MR; Azimzai Y, Batra S, Burford N, Yao MG, Nguyen DB, Lu DAM; Walia NK, Gandhi AR, Au-Young J, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU82012 standard; Protein; 233 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-090431/12.
N-PSDB; ABK28671.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU82012;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 158-159; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JUN-2001; 2001WO-US19862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to forty four human secreted proteins (referred to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; SECP; antiinflammatory; cytostatic; cardiant;
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                           B
                                 89.5%;
85.7%;
                                 Score 34; DB
Pred. No. 51;
                 Mismatches
                                                     23; Length 233;
                 Indels
                 <u>.</u>
                 Gaps
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Search completed: January 12, 2004, 06:58:57 Job time: 17.9531 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                              Score
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38
                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              January 12, 2004, 07:02:25 ; Search time 14 Seconds (without alignments)
100.755 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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Cgn2_6/ptodata/1/pubpaa/US09B PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/US09E PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
Cgn2_6/ptodata/1/pubpaa/US10A PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/US10A PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/US10E PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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110
161
216
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_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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  1 US-09-972-656-13
2 US-09-829-495-65
2 US-10-308-817-117
1 US-09-972-656-130
1 US-10-269-805-52
5 US-10-269-805-52
5 US-10-269-805-58
1 US-09-972-656-108
1 US-09-980-748-1234
1 US-09-925-299-1194
2 US-10-322-673-55
1 US-09-880-748-1842
                                                                                                                                                                                                                                                                                      US-09-832-312-65
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Sequence 65, Appl
Sequence 13, Appl
Sequence 117, App
Sequence 117, App
Sequence 42, Appl
Sequence 52, Appl
Sequence 58, Appl
Sequence 6785, App
Sequence 108, App
Sequence 1194, Ap
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US-10-001-934-50	US-10-001-934-48	US-10-001-934-46	US-10-001-934-44	34-	US-10-001-934-38	US-10-025-687-12	US-09-791-153A-74	US-09-791-153A-8		US-09-880-748-1488	-748-	US-10-039-785-53	-785-	97	US-09-880-748-1965	- 1	US-10-120-414-82	-222-	US-09-880-748-1714	-805-	US-10-269-805-40	-748-	-122	US-09-880-748-1128	8-127	-656-10	-09-972-656-	72-656-	
(D	e 48, App	e 46,	w O	e 42,	e 38,	Œ	e 74,	0	e 1462	e .	e 1540	e 53,	e 53,	e 1974	Sequence 1965, Ap	e 83,	e 82,	e 24, App	e 1714	æ	e 40,	1277	Sequence 1227, Ap	e 1128	e 1273	e 102,	e 90,	20, App	Sequence 14, Appl

# ALIGNMENTS

RESULT 1

US-09-832-312-65

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; Sequence 65, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
PRIOR APPLICATION NUMBER: 09/510,387
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR REFILING DATE: 2000-02-14
; PRIOR REFILING DATE: 1999-10-06-30
; NUMBER FILING DATE: 1999-106-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FASTSEQ FOR Windows Version 3.0
; SEQ ID NO 65
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-65

Query Match
Best Local Similarity 100.0%; Score 38; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.6e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps

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RESULT 2
US-09-972-656-13
; Sequence 13, Application US/09972656
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Query Match
Best Local Similarity
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US-10-308-817-117; Sequence 117, Application US/10308817; Deblication No. US20030219861A1; GENERAL INFORMATION:
; APPLICANT: Rother, Russell; APPLICANT: Wu, Dayang
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; ORGANISM: Homo sapiens
US-09-829-495-65
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PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR PPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
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                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 65
LENGTH: 7
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Publication No. US20040001826A1
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Best Local Similarity 100.0%;
Matches 7; Conservative 0
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APPLICANT: Teai, Mei-Mei
APPLICANT: Trai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/345,468 PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/829,495
CURRENT FILING DATE: 2001-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Busfield SJ
APPLICANT: Villeval J
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ORGANISM: Homo sapiens
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Pred. No.
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US-10-269-805-42
                           Sequence 42, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
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; ORGANISM: human
US-10-308-817-117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 130, Applic publication No. US20 GENERAL INFORMATION:
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SEQ ID NO 117
                                                                  Query Match
Best Local Similarity
Matches 7; Conserv
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SEQ ID NO 130
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Best Local Similarity
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FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma TITLE OF INVENTION: Neutralizing Activity FILE REFERENCE: A-799 CURRENT APPLICATION NUMBER: US/09/972,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
                                                                                                                                                                      LOCATION: (35)..(35)
OTHER INFORMATION: Unidentified NAME/KEY: Wisc.
LOCATION: (36)..(36)
                                                                                                                                                                                                                                                                                               LOCATION: (33)..(33)
OTHER INFORMATION: Unidentified
NAME/KEY: Misc.
                                                                                                                                                         OTHER INFORMATION: Unidentified
                                                                                                                                                                                                                                           NAME/KEY: Misc.
                                                                                                                                                                                                                                                               LOCATION: (34)..(34)
OTHER INFORMATION: Unidentified
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OTHER INFORMATION: Unidentified
NAME/KEY: Misc.
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
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56 EDNORPS 62
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                                  1 EDNQRPS 7
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o. US20030099647A1
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                                                                  100.0%; Score 38; E ilarity 100.0%; Pred. No. 2. Conservative 0; Mismatches
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100.0%; Pred. No. 2:
tive 0; Mismatches
                                                                        Mismatches
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS

FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10

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; SOFTWARE: PatentIn versic
; SEQ ID NO 58
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-269-805-58
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US-10-269-805-52
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; Sequence 58, Application US/10269805
; Publication No. US20030124129A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/10269805
Publication No. US20030124129A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
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NUMBER OF SEQ ID NOS: 76
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CURRENT FILING DATE: 2002-10-10
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 110
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100.0%;
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Pred. No. 2.3;
Score 38;
Pred. No.
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DB 15;
2.3;
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US-09-972-656-108
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CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-3
NUMBER OF SEQ ID NOS: 8564
                                                                                                                                                                                   TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
LENGTH: 216
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. SEQ ID NO 6785
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Best Local Similarity
                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 108, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matchев
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                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al. TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PA005P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 16
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (149)
                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
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                                   EDNORPS 7
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                                                                       Conservative
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                                                                                        100.0%; Score 38; DB 100.0%; Pred. No. 4.6;
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                                                                         Mismatches
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; ORGANISM: Homo sapiens
US-09-880-748-1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1234
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                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1194
LENGTH: 114
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Best Local
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Best Local Similarity
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                                                                         Matches
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
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                                                                                                                                                                                 NAME/KEY: SITE
LOCATION: (108)
                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 EDNORPS 204
37 EDNKRPS 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDNORPS 7
                                1 EDNORPS 7
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                                                                       6,
                                                                       Conservative
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                                                                                          89.5%;
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                                                                                      Score 34; DB
Pred. No. 16;
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RESULT 13

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183 EDNRRPS 189

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; OTHER INFORMATION: CM075A01 SCFV US-10-322-673-55
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US-10-322-673-55
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
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                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/322,673
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/369,877
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-04-05
PRIOR FILING DATE: 2002-06-04
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR APPLICATION NUMBER: 60/386,591
PRIOR APPLICATION NUMBER: 60/396,591
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
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LENGTH: 243
TYPE: PRT
                                              Best Loc
Matches
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Best Local
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                                                                                 Query Match
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                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/425,737 PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TITLE OF INVENTION: Receptors FILE REFERENCE: PF585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 72
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                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
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Local Similarity 85.7%;
1es 6; Conservative
                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/403,370 FILING DATE: 2002-08-15
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    1 EDNORPS 7
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                                              Conservative
                                                            89.5%;
85.7%;
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    Mismatches

                                                                   Score 34;
Pred. No.
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WESULT 15
US-09-880-748-1842
Sequence 1842, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/216,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 92,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                          APPLICATION NUMBER: FR 950591
FILING DATE: 18-MAY-1995
ATTORNEY, AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORES
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Roques, Pierre
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: HIV-1 V
TITLE OF INVENTION: APPLICA
TITLE OF INVENTION: MATERNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Adler, Reid G.
REGISTRATION NUMBER: 30,988
REFERENCE/DOCKET NUMBER: ORE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9505914
FILING DATE: 18-MAY-1995
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ADDRESSEE: MORGAN, L
                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                               APPLICATION NUMBER: US/08/649,991
FILING DATE: 17-MAY-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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          TELEPHONE:
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: 202-467-7000
202-467-7176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEIC ACID FRAGMENTS DERIVED FROM THE HIV-1 VIRUS GENOME, CORRESPONDING PEPTII APPLICATIONS AS REAGENTS FOR EVALUATION MATERNOFOETAL TRANSMISSION OF HIV-1
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eet, N.W.
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                                                                                                                                 FR 9505914
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Pred. No. 33;
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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-649-991-92
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US-09-071-035-344
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                                                                                                              US-09-071-035-344
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Best Local Similarity
Matches 6; Conserv
                                                     Matches
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GENERAL INFORMATION:
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                                                                                  Query Match
                                                                                                                                                                                                              TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES: 496
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CITY: Rockville
                                              56.5%;
Local Similarity 38.5%;
es 5; Conservation
                                                                                                                                                                                                                                                                       NAME: A. Anders Brookes REGISTRATION NUMBER: 36 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: HP Vect
OPERATING SYSTEM:
                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
                                                                                                                                           TOPOLOGY:
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268 TKENSKIANNYIE 280
                         1 TRSSGSIASNYVQ 13
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                                                                                                                                      ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HP Vectra 486,
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                                                                    Score 35;
Pred. No.
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                                                                                  Length 431;
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Search completed: January 12, 2004, 07:04:01 Job time: 12.7656 secs

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RESULT 12
US-08-630-915A-131
; Sequence 131, Application US/08630915A
; Patent No. 6309820
; Patent No. 6309870NI.
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Best Local Similarity
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APPLICANT: ALLIGNET, JEANINE
APPLICANT: ALLIGNET, JEANINE
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS
FILE REFERENCE: 03715-0059
CURRENT APPLICATION NUMBER: US/09/446,301A
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 51
SOCTWARE: PATENTIN VET. 2.1
SEQ ID NO 49
LENGTH: 522
TYPE: DET
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: El Solh, Nevine
APPLICANT: Allignet, Jeanine
APPLICANT: Allignet, Jeanine
TITLE OF INVENTION: POLYNUCLEOTIDES AND THEIR USE FOR DETECTING RESISTANCE
TITLE OF INVENTION: TO STREPTOGRAMIN A OR TO STREPTOGRAMIN B AND RELATED
TITLE OF INVENTION: COMPOUNDS
TILE REFERENCE: 03495.0173-00000
CURRENT APPLICATION NUMBER: U5/09/099,932
CURRENT FILING DATE: 1998-06-19
EARLIER APPLICATION NUMBER: 60/050,380
EARLIER FILING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Staphyloccocus
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38.5%;
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38.5%;
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Pred. No.
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Pred. No. 1.1e+02;
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                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Narwa, Remy
APPLICANT: Roques, Pierre
APPLICANT: Roques, Pierre
TITLE OF INVENTION: HIV-1 V
TITLE OF INVENTION: MATERNO
TITLE OF INVENTION: MATERNO
                                                                                                                                                                                                                                                                                                                                                     sequence 91, Application US/08649991
Patent No. 5919462
COUNTRY: USA
COUNTRY: USA
ZIP: 20036-5869
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPETIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
TITLE OF INVENTION: USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: ur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPHAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 03-APR CLASSIFICATION: 536
                                                                                                                      STATE:
                                                                                                                                     CITY: Washington
                                                                                                                                                        STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.5%;
                                                                                                                                                                                                                               NUCLEIC ACID FRAGMENTS DERIVED FROM THE HIV-1 VIRUS GENOME, CORRESPONDING PEPTIDES AND THEIR APPLICATIONS AS REAGENTS FOR EVALUATION OF THE RISK OF MATERNOFOETAL TRANSMISSION OF HIV-1
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COMPUTER READABLE FORM

OPERATING SYSTEM: MEDIUM TYPE: COMPUTER: IB

IBM Compatible

Diskette

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Query Match
Best Local Similarity
"---hes 8; Conserve
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US-08-232-545-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08232545 Patent No. 6506578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATION:
COMPUTER: PC COMPATION:
COMPATION SYSTEM: PC COMPATION:
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/232,545
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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LENGTH: 505 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/232,545
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ullrich, Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures, Irman G.
TITLE OF INVENTION: No. 6506578el Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
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ATTORNEY/AGENT INFORMATION:
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                   TELECOMMUNICATION INFORMATION:
                                                                                            ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: Pennie &
                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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TOPOLOGY: un
                                       NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 76
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                                                                                                                                                                                                                                                                                                                         CITY: New York STATE: New Yorl
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REGISTRATION NUMBER: 30,742
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ZIP: 10036
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TELEPHONE:
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66.7%;
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Pred. No. 44;
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Best Local Similarity
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ZIP: 10036

COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

COMPUTER: PC-DO
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                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212)869-974:
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
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CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/232,545
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SOFTWARE: PATENTIN Release #1.0, ...
CURRENT APPLICATION DATA: PCT/US95/05008
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                                                                                                                                                                                              TOPOLOGY: u
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FILING DATE: 22-APR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
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Y: U.S.A.
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1155 Avenue of the Americas
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(212)869-9741
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Redwood City, California 94063-4720
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66.7%;
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                              61.3%; Score 38; DB 5; 66.7%; Pred. No. 44; tive 0; Mismatches
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                                                                                                    Length 505;
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RESULT 6
US-08-362-780-26
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Patent No. 5
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Best Local Similarity 66.7%;
Matches 8; Conservative
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NFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: 07/862,543

FILING DATE: 23-UUNE-1992

APPLICATION NUMBER: GB 9021679.7

FILING DATE: 05-OCT-1990

PRIOR APPLICATION NUMBER: WO PCT/GB91/01726

APPLICATION NUMBER: WO PCT/GB91/01726
                                                                                                                                                                                                                                                                                                                                        NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,780
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APPLICANT: Waldmann, Herman
TITLE OF INVENTION: Antibody Preparation
NUMBER OF SEQUENCES: 26
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                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
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TO NO TO N
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CLASSIFICATION: 424
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STATE: Virginia
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                                                             TLSSGNIENNYV 34
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8th Floor, 1100 No. 5968509th Glebe Road
                                                                                                                          Conservative
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                                                                                                                                                                                                                    linear
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                                                                                                                                        62.9%;
                                                                                                                                       Score 39;
Pred. No.
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Pred. No.
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                                                                                                                                                     Length 110
                                                                                                                          Indels
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RESULT 7
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; MOLECULE TYPE: peptide
US-08-362-780-26
                                                                                                                                                                                                                                                                   US-08-426-509A-17
                                                                                                                                                                                                            Sequence 17, Application US/08426509A Patent No. 6326469 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 26, Application US/08362780 Patent No. 5968509 GENERAL INFORMATION:
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,543
PILING DATE: 23-UNB-1992
APPLICATION NUMBER: GB 9021679.7
PILING DATE: 05-OCT-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB91/01
PILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edwar
APPLICANT: waldmann, Hermar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,780
FILING DATE:
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                    APPLICANT: Gishizsky,, Mikhail
APPLICANT: Sures,, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
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APPLICANT: Waldmann, Herman
TITLE OF INVENTION: Antibody Preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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TELEPHONE: 7038164100
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STATE: Virginia
COUNTRY: USA
                    STATE:
                                                   STREET:
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COUNTRY:
                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
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8; Conserv
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8th Floor, 1100 No. 5968509th Glebe Road
 USA
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Pred. No. 4.9;
2; Mismatches
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4.9;
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Patent No. 5968509
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INFORMATION FOR SEQ ID NO:
                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/362,780
FILING DATE:
CLASSIFICATION: 424
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APPLICATION NUMBER: GB 9206422.9
FILING DATE: 24 MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB92/01933
FILING DATE: 21-0CT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/862,543
FILING DATE: 23-JUNE-1992
APPLICATION NUMBER: GB 9021679
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: Antibody Préparation
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Local Similarity 66.7%;
nes 8; Conservative
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Y: USA
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8th Floor, 1100 No. 5968509th Glebe Road
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 GB 9021679.7
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Pred. No. 0.
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US-07-988-925-16
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SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: Bingle
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; Patent No. 55850;
; GENERAL INFORMA
APPLICANT: E
; APPLICANT: C
APPLICANT: C
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Best Local Similarity
                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMERR. GB 920642
PILING DATE: 24-MAR-1992
PRIOR APPLICATION UNMERR. WO PCT/GE
PILING DATE: 21-OCT-1992
APPLICATION UNMERR. WO PCT/GE
PILING DATE: 21-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29009
TELECOMMUNICATION IMFORMATION:
TELECOMMUNICATION IMFORMATION:
                                            TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/988,925
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REGISTRATION NUMBER: 29009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
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FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-OCT-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: antibody preparation
NUMBER OF SEQUENCES: 24
                                                                     TELEPHONE: 7038164100
                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
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STRANDEDNESS:
                             ENGTH:
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                amino acid
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11th Floor, 1100 No. 5585097th Glebe Road
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Clark, Michael R
                             110 amino acids
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Pred. No. 0.42;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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             Pred. No. is the number of results predicted by chance to n score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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seq length: 2000000000
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/cgn2_6/ptodata/2/iaa/BCTUS_COMB.pep:*
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     PCT-US95-05008-16
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US-08-233-389C-9
US-08-801-863-9
US-08-486-596A-9
US-09-004-713-9
US-08-619-841-2
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US-08-362-780-16
US-08-362-780-26
US-08-322-545-17
PCT-US-95-05-008-17
US-09-446-301A-49
US-09-099-932-49
US-08-630-915A-131
US-08-649-991-91
US-08-649-991-92
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Sequence 64, Appl Sequence 4, Appl is Sequence 4, Appl is Sequence 16, Appl is Sequence 26, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 19, Appl Sequence 19, Appl Sequence 314, Appl Sequence 342, Appl Sequence 342, Appl Sequence 342, Appl Sequence 16, Appl Sequence 17, Appl Sequence 17, Appl Sequence 18, Appl Sequence 2, Appli Sequence 9, Appli
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54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8
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PCT-US95-08743-147	US-09-025-769B-51	US-09-025-769B-32	US-09-240-274-59	US-08-899-575-147	US-08-899-575-147	US-08-276-852-147	US-08-635-109-5	US-09-315-574-38	US-08-665-202-38	US-08-211-202-111	US-09-461-325-222	US-07-776-272-20	5424221-4	US-09-070-504-9	US-09-070-504-8	US-09-070-504-3	US-08-446-929A-2
Sequence 147, App	Sequence 51, Appl	Sequence 32, Appl	Sequence 59, Appl	Sequence 147, App	Sequence 147, App	Sequence 147, App	Sequence 5, Appli	Sequence 38, Appl	Sequence 38, Appl	Sequence 111, App		Sequence 20, Appl	Patent No. 5424221	Sequence 9, Appli	Sequence 8, Appli	Sequence 3, Appli	Sequence 2, Appli

#### ALIGNMENTS

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RESULT 2
US-07-988-925-4
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-64
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TITLE OF INVENTION: GLYCOPROTEIN VI AND USES TH
FILLE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
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SOFTWARE: FAB
; SEQ ID NO 64
; SEQTH: 13
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Matches 13
                                                                                                                                                                                                                         Sequence 4 Patent No.
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                                                                          GENERAL INFORMATION:

APPLICANT: Bolt, Sarah L
APPLICANT: Clark, Michael R
APPLICANT: Gorman, Scott D
APPLICANT: Routledge, Edward G
APPLICANT: Waldmann, Herman
TITLE OF INVENTION: antibody preparation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/345,468
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                       ADDRESSEE:
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5. 5585097
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11th Floor, 1100 No. 5585097th Glebe Road
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Pred. No. 2.4e-05;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: January 12, 2004, 06:54:49; Search time 11.7812 Seconds (without alignments) 106.117 Million cell updates/sec

Title: Perfect score: US-09-829-495-64 62

Scoring table: TRSSGSIASNYVQ 13

BLOSUM62 Gapop 10.0 , Gapext 0.5 283308 seqs, 96168682 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000,

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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scor	Query e Match	Length	1 ! BB	ID	scription
2 L 5	88	112 131		품품	bda cha bda cha
٠ س	1 82.	111	_	L6HULT	lambda
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ω	8 61.	112	<u>_</u>	L6HUAR	lambda
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ω	6 58.	140	N	H86292	8 protei
w	σ	308	2	G90504	2-keto-3-deoxy glu
ω	6 58.	352	N	T27677	tical p
w	6 58.	522	N	JC1204	- 1
w	6 58.	539	ν	B49114	ein-tyrosi
ω	σ	549	N	S61706	RNA 5'-triphospha
u	6 58.	997	N	T15243	hypothetical p
ω	5 56.	131	N	S24321	Ig lambda chain pr
w	5 56.	278	N	T39517	n
u	5 56.	402	N	C69110	glutamate N-acet
u	5 56.	503	<b>ب</b>	JQ1321	protein-tyrosine
w	5 56.	503	_	TVMSHC	protein-tyrosine
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Ig lambda chain precursor V-VI region (EB4) - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C;Accession: A01990
R;Anderson, M.L.M.; Brown, L.; McKenzie, E.; Kellow, J.E.; Young, B.D.
Nucleic Acids Res. 13, 2931-2941, 1985
A;Title: Cloning and sequence analysis of an Ig lambda light chain mRNA expressed in the A;Reference number: A01990; MUID:85215660; PMID:3923440
A;Rocession: A01990
A;Rocession: A01990
A;Rocession: A01990
A;Residues: 1-131 <AND>

A;Gene: GDB:IGLV@ A;Cross-references: GDB:119342; OMIM:147240 A;Map position: 22q11.2-22q11.2

C; Genetics:

<b>4</b> 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	3 <u>1</u>	30
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54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	54.8	56.5	56.5	56.5	56.5	56.5	56.5	56.5
130	129	127	124	98	97	72	55	47	1167	1007	859	788	788	574	541
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
S78057	S78058	A25864	C48234	S36048	D89792	137232	PQ0829	B30607	T06146	H81670	AE2217	F97547	AC2767	T40213	S31645
Ig lambda chain pr	Ig lambda chain pr	calcitonin gene-re	hypothetical prote	Ig lambda chain -	conserved hypothet	calcitonin gene-re	E2/NS1 protein (cD	Ig kappa chain V-I	disease resistance	conserved hypothet	hypothetical prote	probable oxidoredu	formate dehydrogen	hypothetical prote	protein-tyrosine k

## ALIGNMENTS

Query Match 83.9%; Score 52; DB 1; Length 112; Best Local Similarity 84.6%; Pred. No. 0.016; Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps  Qy 1 TRSSGSIASNYVQ 13	A;Gene: GDB:IGLV@ A;Cross-references: GDB:119342; OMIM:147240 A;Cross-references: GDB:119342; OMIM:147240 A;Map position: 22q11.2-22q11.2 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer C;Keywords: heterotetramer F;15-93/Domain: immunoglobulin homology <imm'> F;22-91/Disulfide bonds: #status predicted</imm'>	A;Molecule type: protein A;Residues: 1-112 <tak> A;Residues: 1-112   A;Note: this is the first sequenced V region of lambda chain subgroup VI C;Comment: This is a Bence Jones protein. C;Genetics:</tak>	R;Takahashi, N.; Takayasu, T.; Isobe, T.; Shinoda, T.; Okuyama, T.; Shimizu, A. J. Biochem. 86, 1523-1535, 1979 J. Biochem. 86, 1523-1535, 1979 A;Title: Comparative study on the structure of the light chains of human immunoglobulins A;Reference number: A01991; MUID:80094390; PMID:118171 A;Accession: A01991	RESULT 1 1.6HU48 Ig lambda chain V-VI region (Nig-48) - human C;Species: Homo sapiens (man) C;Date: 28-Feb-1980 #sequence_revision 28-Feb-1980 #text_change 02-Sep-1997
	dentical light ()	up VI	Shimizu, A. human immunoglobul	Sep-1997

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F;42-54/Region: c
F;55-69/Region: f
F;70-76/Region: c
F;77-110/Region:
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F;51-57/Region:
F;58-91/Region:
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C; Keywords: heterotetramer;
F;1-22/Region: framework I;
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A;Molecule type: protein
A;Residues: 1-111 <DWU>
C;Genetics:
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A;Title: Amino acid sequence of a lambda VI primary (AL)
A;Reference number: A01989; MUID:86122667; PMID:4089539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;111-118/Region: complementarity-determining
F;119-131/Region: framework 4
F;41-110/Disulfide bonds: #status predicted
                                          Ig lambda chain V-VI region (SUT) - human (;Species: Homo sapiens (man) C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 C;Accession: A01988
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A;Cross-references: GDB:119342; OMIM:147240
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                         R;Solomon,
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;1-19/Domain: signal sequence #status predicted <SIG>
;20-131/Product: Ig lambda chain V-VI region (EB4) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kapain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lassuperfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
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:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
:Accession: A01989
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-35/Region:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lambda chain V-VI region (WLT) - human
A.; Kyle, R.A.; Frangione, B.
losis, Glenner, G.G., Osserman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42
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                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                 TGSSGSIGSNYVQ 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complementarity-determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             framework 2
                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               #status predicted
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84.6%;
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Pred. No. 0.02
0; Mismatches
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Pred. No. 0.019;
1; Mismatches
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  E.F.,
                                                                                                                                                                                                                                                                                                                                             DB 1;
0.025;
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  Benditt,
                                                                 #text_change 02-Sep-1997
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  E.P.,
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    Calkins,
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    Cohn,
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    A.S.,
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Ig lambda chain V-VI region (AR) - human (tentative seque C; Species: Homo sapiens (man)
C; Abate: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_C; Accession: A01987
R; Sletten, K.; Natvig, J.B.; Husby, G.; Juul, J.
Biochem. J. 195, 561-572, 1981
A; Title: The complete amino acid sequence of a prototype A; Reference number: A01987; MUID:82091000; PMID:6797401
A; Contents: amyloid protein AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-778 <GEN>
A;Residues: 1-778 <GEN>
A;Cross-references: EMBL:Z98981; PIDN:CAB11736.1; GSPDB:GN00066; SPDB:SPAC6F6.13c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SPAC6F6.13c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000 C;Accession: T39047
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, September 1997
A;Reference number: Z21797
A;Accession: T39047
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la c;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;1-22/Region: framework 1
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A;Accession: A01988
A;Molecule type: protein
A;Residues: 1-111 <SOL>
C;Genetics:
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F;51-57/Region: complementarity-determining
F;58-91/Region: framework 3
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C; Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;92-100/Region: complementarity-determining;101-111/Region: framework 4
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Best Local
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8; Conserv
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72.7%;
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Pred. No. 0.
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Pred. No.
                                                                                                                                                                                               human (tentative sequence)
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immunoglobulin-lambda light-cha

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A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate int C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: amyloid; heterotetramer; immunoglobulin F;15-93/Domain: immunoglobulin homology cIMM>
F;22-91/Disulfide bonds: #status predicted
A;Cross-references: GDB:119303; OMIM:142370
A;Map position: 20q11-20q12
A;Introns: 207/1; 258/1; 318/1; 343/3; 395/1; 439/1
C;Function:
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
A;Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
C;Superfamily: protein-tyrosine kinase src; protein kinase homology; SH2 homology; SH3
C;Keywords: ATP; autophosphorylation; blocked amino end; lipoprotein; myristylation; pt
F;2-505/Product: protein-tyrosine kinase hck #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                        R;Partanen, J.; Maekelae, T.P.; Alitalo, R.; Lehvaeslaiho, H.; Alitalo, K. Proc. Natl. Acad. Sci. U.S.A. 87, 8913-8917, 1990
A;Title: Putative tyrosine kinases expressed in K-562 human leukemia cells. A;Reference number: A38268; MUID:91062389; PMID:2247464
A;Accession: C38268
A;Status: nucleic acid sequence not shown; not compared with conceptual transportations: 362-417 <PAR>
A;Residues: 362-417 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein-tyrosine kinase (EC 2.7.1.112) hck - human C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Dec-1989 #sequence revision 10-Nov-1995 #text_change 11-Jun-1999 C;Accession: A27811; A27812; \(\overline{JC}(1149); C38268; S31103\)
R;Quintrell, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, Mol. Cell. Biol. 7, 2267-2275, 1987
Mol. Cell. Biol. 7, 2267-2275, 1987
A;Title: Identification of a human gene (HCK) that encodes a protein-tyrosine k A;Reference number: A27811; MUID:87257942; PMID:3496523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1-112 <SLE>
A; Residues: 1-112 <SLE>
A; Rote: about half of the lambda chain C region is missing from this protein
C; Comment: This protein was isolated from the spleen of a patient with amyloidosis.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 157-505 - HRA>
A; Cross-references: EMBL: X59741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M16592; NID:g183913; PIDN:AAA52644.1; R;Hradetzky, D.; Strebhardt, K.; Ruebsamen-Waigmann, H. Gene 113, 275-280, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: the codon given for 3-Cys (TCG) is inconsistent with the authors' R;Ziegler, S.F.; Marth, J.D.; Lewis, D.B.; Perlmutter, R.M. Mol. Cell. Biol. 7, 2276-2285, 1987
A;Title: Novel protein-tyrosine kinase gene (hck) preferentially expressed A;Reference number: A27812; MUID:87257943; PMID:3453117
A;Accession: A27812
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Best Local S
Matches 8
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Residues: 1-505 < QUI>
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7.2;
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conserved hypothetical protein VCA1085 [imported] - Vibrio cholerae (strain
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82379
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F;123-220/Domain: SH2 homology <SH2>
F;123-220/Domain: SH2 homology <SH2>
F;239-497/Domain: protein kinase homology <KIN>
F;247-255/Region: protein kinase ATP-binding motif
F;247-255/Region: protein kinase ATP-binding motif
F;247-255/Region: protein kinase ATP-binding motif
F;247-255/Region: protein kinase homology <KIN>
F;247-255/Region: protein kinase homology <KIN
F;247-25
A;Map position: 5
A;Introne: 4/3; 76/1; 144/1; 226/3; 400/2; 446/1; 562/3
C;Superfamily: glucose transport protein
                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-606 <WIL>
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C;Date: 15-Oct-1999 #sequence_rev
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A;Molecule type: DNA
A;Residues: 1-556 <HEI>
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A;Accession: B82379
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                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T27072
                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A;Reference number: Z20307
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                                                                                                                A;Gene: CESP:Y51A2D.4
                                                                                                                                                                                                                             A;Cross-references: EMBL:AL021497; PIDN:CAA16400.1; GSPDB:GN00023; CESP:Y51A2D.
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36;
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I.; Sellers,
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Query Match Best Local S Matches 7

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61.3%;

Conservative

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hypothetical protein ECs1137 [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli (c;Cate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: A90771 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen A;Accession: A90771 A;Accession: A90771 A;Accession: A90771 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE005174; NID:g12514246; PIDN:AAG55529.1; GSPDB:GN00145; A;Experimental source: strain O157:H7, substrain EDL933 C;Genetics:
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A; Residues: 1-726 <HAY>
A; Cross-references: GB: BA000007; PIDN: BAB34560.1; PID: 913360597;
A; Experimental source: strain O157: H7, substrain RIMD 0509952
C; Genetics:
probable ATPase yccC - Escherichia coli (strain K-12) C;Species: Escherichia coli (c;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #t C;Accession: C64839 #t C;Accession: C64839 #t III, G.; Bloch, C.A.; Pern R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pern A; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein yccC [imported] - Escherichia coli (strain C;Species: Escherichia coli C;Species: Escherichia coli C;Pate: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change C;Pate: 16-Peb-3001 #sequence_revision 16-Feb-2001 #text_change C;Accession: E85633 C;Pate N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
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                         G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley,
Y.
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Pred. No. 48;
2; Mismatches
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Pred. No.
                                                                                  17-Sep-1997 #text_change 01-Mar-2002
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A;Title: The complete genome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503 A;Accession: C64839 A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA A;Residues: 1-726 <BLAT> A;Residues: 1-726 <BLAT> A;Cross-references: GB:AE000200; GB:U00096; NID:g2367111; 1A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: PS0073
A;Status: translation not shown
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-108 <LEV>
C;Superfamily: immunoglobulin V region;
C;Keywords: heterotetramer; immunoglobul
F;16-91/Domain: immunoglobulin homology
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C;Keywords: ATF; nucleotide binding; P-loop; transmembrane
F;34-50/Domain: transmembrane #status predicted <TM1>
F;428-444/Domain: transmembrane #status predicted <TM2>
F;539-546/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Levy, S.; Campbell, M.J.; Levy, R.
J. Exp. Med. 170, 1-13, 1989
A;Title: Functional immunoglobulin light chain genes are
A;Reference number: A92781; MUID:89310348; PMID:2501443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision
C;Accession: PS0073
                                                                                                                                                                                                                            R;Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, J. Bacteriol. 181, 6509-6515, 1999
A;Title: Sequence and organization of pXO1, the large Bacillus anthracis plantare processing and process plantary part of pxo1, MID:10515943
                                                                                                                                                                                                                                                                                                                                         hypothetical protein pXO1-61 - Bacillus anthracis virulence plasmid pXO1 C;Species: Bacillus anthracis C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 16-Feb-2001
                                                                                              A;Cross-references: GB:AF065404; NID:g4894216; A;Experimental source: strain Sterne
                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-236 <OKI>
  C; Superfamily:
                                          A,Gene: pXO1-61
                                                                                     A; Experimental source:
                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                                         A;Accession: E59098
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Mus musculus (house mouse)
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hypothetical protein pXO1-61
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Score 37;

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Length

Koehler

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C;Genetics:
A;Gene: myoC
A;Introns: 307/1
C;Superfamily: protozoan myosin heavy chain IB; myosin motor domain homology; SH3 homology; F;18-685/Domain: myosin motor domain homology <MMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin IC - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 08-Sep-2000
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Search completed: January 12, 2004, 07:03:04 Job time: 14.7812 secs
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R;Peterson, M.D.; Novak, K.D.; Reedy, M.C.; Ruman, J.I.; Titus, M.A.
J. Cell Sci. 108, 1093-1103, 1995
A;Title: Molecular genetic analysis of myoC, a Dictyostelium myosin I.
A;Reference number: Z20872; MUID:95348228; PMID:7622596
A;Accession: T30578
                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1181 <PET>
A;Cross-references: EMBL:L35323; NID:g532123; PID:g532124; PIDN:AAC37427.1
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Best Local Similarity 53.8
Matches 7; Conservative
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25 KDSGSLLTNYVE 36
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3 mus musculu
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RESULT 2 LV6E_HUMAN

SCHOOL

TAV6E HUMAN STANDARD; PRT; 131 AA. P06319; 01-JAN-1988 (Rel. 06, Created) 01-JAN-1988 (Rel. 06, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 lambda chain VVI region EB4 precursor. Homo sapiens (Human).

D Qy	3 W Q	THE SECOND SECON	RESULT LV6B_H ID L AC P		
	Query Match Best Local Matches 1	21-JUL-1986 (Rel. 15-SEP-2003 (Rel. 19 lambda chain V Homo sapiens (Hum Bukaryota; Metazo Mammalia; Eutheri (I) SEQUENCE: SEQUENCE: MEDLINE-80094390; Takahashi N., Tak Shimizu A.; "Comparative stud immunoglobulins. J. Biochem. 86:15!- MISCELLANEOUS "COMPARTITY: CO PIR; A01991; L540U HSSP; P01703; 7FA GO; GO:0003823; FC GO; GO:00038	ULT 1 B_HUMAN LV6B_H P01722		66666666666666666666666666666666666666
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	re 52; DB d. No. 0.0 Mismatches	puence update) iotation update G-48. Craniata; Vert. Catarrhini; Ho Catarrhini; Ho be T., Shinoda cture of the 1 lit of a new sub sence-Jones pro unoglobulin-li ir; NAS. ling activity; l	112	ALIGNMENTS	HORSE HORSE BOVIN HUMAN
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HSSP; P01709; 2MCG.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000553; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0077110; I3-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; ig; 1.
SMART; SM00406; IGv; 1.
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GO; GO:0003623; F:antigen binding activity;
GO; GO:0006955; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_WHC.
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01-JAN-1988 (Rel. 06, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig lambda chain V-VI region WLT.
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PROSITE; PS5085; IG LINE
PROSITE; PS5085; IG LINE
PROSIT
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                                                                                                                                                                                                                                                                                                                                 MEDLINE=86122667; PubMed=4089539;
Dwulet F.E., Strako K., Benson M.D.;
"Amino acid sequence of a lambda VI
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Mammalia; Eutheria;
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HSSP; P01709; 2MCG.
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Mammalia; Eutheria;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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Pred. No. 0.0041;
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BY SIMILARI
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cohen A.S., Zucker-Franklin D. (ed
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"Light chain variable region subgroups
in amyloidosis AL.";
(In) Glenner G.G., Osserman E.F., Bendi
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01-JAN-1988 (Rel. 06, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig lambda chain V-VI region SUT.
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PIR; A01988; L6HUST.
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COMPLEMENTARITY-DETERMINING-3
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1.
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RESULT 6
HCK_MACFA
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Best Local
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P01721;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain V-VI region AR.

Sukaryota; Meta?~~

lammal'-
                                    Thesis (2001), University of Marseille, France.
-!- FUNCTION: MAY SERVE AS PART OF A SIGNALING RATHWAY COUPLING RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALS CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sletten K., Natvig J.B., Husby G., Juul J.;
"The complete amino acid sequence of a prototype
immunoglobulin-lambda light-chain-type amyloid-fibril protein
                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
27-FEB-2003 (Rel. 41, Last amotation update)
Lyrosine-protein kinase HCK (EC 2.7.1.112) (p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. J. .195:561-572(1981)
                                                                                                                                                                                                                                                                             Q95M30;
                                                                                                                                                                                                                                                                                        HCK_MACFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01987; L6HUAR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    Picard
                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                    NCBI_TaxID=9541;
                                                                                                                                                 Cercopithecinae; Macaca.
                                                                                                                                                                                        Macaca fascicularis
                                                                                                                                                                                                                 kinase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=82091000; PubMed=6797401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE (AMYLOID PROTEIN AR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mmunoglobulin V region; Amyloid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity;
GO:0006955; P:immune response; NAS.
erPro; IPR007110; Ig-like.
erPro; IPR003006; Ig_MHC.
erPro; IPR03596; Ig_v.
tyrosine phosphate.
SUBCELLULAR LOCATION: Membrane-associated (By similarity)
                        CATALYTIC ACTIVITY: ATP + a protein tyrosine =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PATIENT WITH AMYLOIDOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AA; 11918 MW; 570BCD9A368EF1FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                Primates;
                                                                                                                                                                          Chordata;
                                                                                                                                                                                        (Crab
                                                                                                                                                                                                                                                                                                                                                                                                                   61.3%;
                                                                                                                                                             eating macaque) (Cynomolgus monkey).
ata; Craniata; Vertebrata; Euteleostomi;
tes; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin-like domain
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Pred. No.
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                                                                                                                                                                                                                           (p56-HCK) (Hemopoietic cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
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RESULT 7
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Prodom; PD000093; SH2; 1.
Prodom; PD000066; SH3; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH3; 1.
SMART; SM00219; TyrKC; 1.
SMART; SM00219; TyrKC; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00109; PROTEIN KINASE TYR; 1.
PROSITE; PS50001; PROTEIN KINASE DOM; 1.
PROSITE; PS50001; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; T.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
                                                                                                    HCK_HUMAN STANDARD; PRT; 526 AA.

P08631; Q96CC0; Q9H5Y5; Q9NUA4; Q9UMJ5;

01-AUG-1988 (Rel. 08, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Tyrosine-protein kinase HCK (EC 2.7.1.112) (p59-HCK/p60-HCK)
                                                                                                                                                                                                                                                                                                                                                                               NP BIND
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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between the Swiss Institute of Bioinformatics and the EMBL
SEQUENCE OF 22-526 FROM N.A.
MEDLINE=87257942; PubMed=3496523;
                                  NCBI_TaxID=9606;
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InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ320181; CAC44031.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
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                                                                        Homo sapiens (Human)
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SIMILARITY: Contains 1
SIMILARITY: Contains 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2
                                                                                                                                                                                                                                                                                                                                504 AA;
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                                                                                                cell kinase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                             domain;
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219
493
254
268
359
                                              Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                 57096
                                                                                                                                                                                                                                                                                           61.3%;
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SH3 domain.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CYCLOTOLOGY. (ATTO.)
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Pred. No.
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                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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(See http://www.isb-sib.
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RX MEDLINE-21638749; PubMed=11780052;
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA Deloukas P., Matthews E.H., Ashurst J., Babbage A.K., Bagguley C.L.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Beasley O.P., Bird C.P., Blakey S.E., Dridgeman A.M., Brown A.J.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
Collec C.M., Coville G.J., Deadman R., Dhami P.D., Dunn M.
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.
RA Coulson A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Huckle E., Hunt A.R., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Shuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Teet L., Thomas D.W., Thorpe A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
RA Whitehead S.L., Whittaker P., Willey D.L., Williams S.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Allschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RICHARD S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Hollon E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Fahey J., Hollon B., Ketteman M., Maran M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
Thuman and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Kawakami T., Noguchi S., Itoh T., Shigeta K., Senk
Kawakami T., Noguchi S., Itoh T., Shigeta K., Senk
Nakajima Y., Mizuno T., Morinaga M., Tanigami A.,
Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.
Obayashi M., Nishi T., Shibahara T., Tanaka T., Na
Isogai T., Sugano S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quintrell N., Lebo R., Varmus H., Bishop J.M., Pettenati M.J., le Beau M.M., Diaz M.O., Rowley J.D.; le Beau M.M., Diaz M.O., Rowley J.D.; life the protein-tyrosine "Identification of a human gene (HCK) that encodes a protein-tyrosine kinase and is expressed in hemopoietic cells."; Mol. Cell. Biol. 7:2267-2275(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22388257; PubMed=12477932;
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TISSUE=B-cel
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1. Biol. 7:2276-2285(1987)
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EMBL/GenBank/DDBJ
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Gmeiner W.H., Byrd R.A.;
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Arold S., O'Brien
Ladbury J.E.;
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"Crystal structure of the
Nature 385:602-609(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-22 FROM N.A., AND A MEDILINE=91342636; PubMed=1875927; MEDILINE=9134636; PubMed=1875927; MEDILINE=9134636; PubMed=1875927; Stanley E. Stanle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene
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"The genomic locus of the human hemopoletic-specific
tyrosine kinase (PTK) encoding gene (HCK) confirms co
exon-intron structure among human PTKs of the scr fam
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[6]
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"The DNA sequence and comparative Nature 414:865-871(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequential assignment and secondary structure determination Src homology 2 domain of hematopoietic cellular kinase."; FEBS Lett. 406:131-135(1997).

1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLI RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE DEGRANULATION PROCESS OF NEUTROPHILS.

1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97263487; PubMed=9109402; Zhang W., Smithgall T.E., Gmeiner W.H.;
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MEDLINE=98453315; PubMed=9778343;
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domains for HIV-1 Net
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                                                                                                                                    Event-Alternative initiation;
Comment=2 isoforms, p60-HCK (shown he produced by alternative initiation;
ITISSUE SPECIFICITY: EXPRESSED PREDOMINA MYELOID AND B-LYMPHOID LINEAGES.
SIMILARITY: BELONGS TO THE TYR FAMILY OUBFAMILY.
SIMILARITY: Contains 1 SH2 domain.
SIMILARITY: Contains 1 SH3 domain.
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similarity).
ALTERNATIVE PRODUCTS:
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SUBCELLULAR LOCATION: Isoform
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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he Src family tyrosine kinase
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                         SEQUENCE FROM N.A., SEQUENCE OF 1-17, AND CHARACT STRAIN-0127:H6 / E2348/69;
MEDLINE=99298177; PubMed=10369665;
Ilan O.A., Bloch Y., Frankel G., Ullrich H., Geid "Protein tyrosine kinases in bacterial pathogens virulence and production of exopolysaccharide.";
EMBO J. 18:3241-3248(1999)
                                                                                                                                                                                                                                                                                                                      SMART; SM00252; SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                 Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send
                                                                                                 NCBI_TaxID=168807;
                                                                                                            Enterobacteriaceae;
                                                                                                                     Bacteria;
                                                                                                                                 Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                            interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0004713; F:protein tyrosine kinase ac
GO:0007498; P:mesoderm development; TAS:
GO:0006468; P:protein amino acid phospho
erPro; IPR000719; Prot kinase.
erPro; IPR000980; SH2.
                 CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                               EC027
SUBCELLULAR
         tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4HCK;
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3HCK; 15-OCT-97.
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                                                                                                                     Proteobacteria;
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IPR001245; Tyr_
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08-JUN-99.
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                                                                                                                                                          (Rel. 41, Created)
(Rel. 41, Last sequence up)
(Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                               STANDARD;
LOCATION: Inner membrane
                                                                                                                                                 kinase etk (EC
                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                          61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                           Tyr_pkinase.
se; 1.
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                                                                                                                     Gammaproteobacteria;
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Pred.
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ptation update)
c 2.7.1.112).
                protein tyrosine = ADP + protein
                                                                                 1-17, AND CHARACTERIZATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorylation; TAS
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RESULT 9
ETK_ECO57
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Q8XC28;
28-FEB-2003
                                                                                                                                                                                                                                                                                                                                                 STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatri Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Mil Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potam Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz Welch R.A., Blattner F.R.;
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SEQUENCE
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                                                                                                              STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino K., Ohnishi K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Ruhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

PNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Tyrosine-protein kinase etk (EC 2.7.1.112).
ETK OR Z1398 OR ECS1137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collat between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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STRAIN=0157:H7 / E
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Transferase; Tyrosine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                     Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                       Genome sequence of enterohaemorrhagic
                                                 SUBCELLULAR LOCATION: Inner membrane (By s
PTM: Autophosphorylated. Dephosphorylated
SIMILARITY: BELONGS TO THE ETK/WZC FAMILY.
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                                                                                                   tyrosine phosphate.
                 SWISS-PROT entry
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Pred. No.
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Kirkpatrick H.A.,
ihao Y., Miller L.,
E.T., Potamousis K.,
Schwartz D.C.,
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Tobe T.,
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RESULT 10
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01-NOV-1997 (Re.
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                          "The complete nucleotide sequence of reveals significant homology between glucose-1-phosphatase."
J. Bacteriol. 172:5497-5500(1990).
                                                                                                                                                                                           Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE005292; AAG55529.1; -.
EMBL; AP002524; BAB34560.1; -.
PIR; A90771; A90771.
PIR; E85633; E85633.
                                                                                      SEQUENCE OF 628-726 FROM N.A. MEDLINE=90368616; PubMed=2168385; Dassa J., Marck C., Boquet P.L.;
                                                                                                                                                "A 718-kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region DNA Res. 3:137-155(1996).
                                                                                                                                                                                                                                                                                                      STRAIN=K12;
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Enterobacteriaceae; Escher
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IDENTIFICATION
                                                                                                                                                                                                                                                                                         MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inner
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MEM 33 53 POTEN
MEM 425 445 POTEN
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RESULT 11
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OS HOMO 9
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EMBL; D90735; BAA35746.1; --
EMBL; M9708; -; NOT ANNOTATED_CDS
EMBL; M5708; - C64839;
PIR; C64839; C64839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as modified and this statement is not removed. Use entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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Vincent C., Duclos B., Grangeasse C.,
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"Intrinsic and extrinsic
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EcoGene; EG11826; etk.
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SMEM 425
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tion of ZNF291,
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Genew; HGCC:13081; ZnF_C2H2.

InterPro; IPR007087; Znf_C2H2.

SMART; SM00355; ZnF_C2H2; 1.

PROSITE; PS01052; ZINC_FINGER_C2H2_1; 1.

PROSITE; PS0157; ZINC_FINGER_C2H2_2; FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                     Peterson M.D., Novak K.D., Reedy M.C., Ruman J.I., Titus M.A.;
"Molecular genetic analysis of myoC, a Dictyostelium myosin I.";
J. Cell Sci. 108:1093-1103(1995).
-I- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN:
-I- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIMER OF A HEAVY
AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.
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01-NOV-1995 (Rel. 32, Last seg
16-OCT-2001 (Rel. 40, Last ann
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01-NOV-1995
                                                  InterPro; IPR001609; myosin_head.
InterPro; IPR000108; Neu_cyt_fact_2.
InterPro; IPR001452; SH3
                                                                                                                                             EMBL; L35323; AAC37427.1; PIR; T30578; T30578.
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Eukaryota; Mycetozoa; Dic
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             PF00063; myosin_head; 2.
PF00018; SH3; 1.
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PR00193; MYOSINHEAVY
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Dictyosteliida; Dictyostelium.
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
SERAIN=cv. Columbia;
STRAIN=cv. Columbia;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
SRIKEN Arabidopsis full length cDNA clones (RAFLS) sequenced )
"RIKEN Arabidopsis full length CDNA clones (RAFLS) sequenced )
SSP consortium (Salk/Stanford/PGEC).";
SSP consortium (Salk/Stanford/PGEC).";
SSP consortium (Salk/Stanford/PGEC).";
SSP consortium (Salk/Stanford/PGEC).";
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Q9LHE5;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable mitochondrial import receptor subunit TOM40 homolog
(Translocase of outer membrane 40 kDa subunit homolog).
TOM40 OR AT3G20000 OR MZE19.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NP_BIND
DOMAIN
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ProDom; PD000066; SH3; 1
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                  "Purification and characterization of the preprotein translocase the outer mitochondrial membrane from Arabidopsis thaliana. Identification of multiple forms of TOM20."; plant Physiol. 125:943-954 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20363099; PubMed=10907853; Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.; "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4,251,695 bp regions covered by 90 Pl, 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; edicottyledons; core eudicots; Rosid.

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                MEDLINE=21608403; PubMed=11743114;
Kruft V., Eubel H., Jaensch L., We
                                                                                                                                                                                     SEQUENCE OF 1-15 AND 246-258, AND SUBCELLULAR LOCATION TISSUE-Leaf, and Stem;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Werhahn W., Niemeyer A., Jaensch L., Kruft V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11161051;
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                                                                         Proteomic approach to identify novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC clones.";
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   Physiol. 127:1694-1710(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKQIGMLPSNYVQ 1179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7:217-221 (2000).
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1181 AA; 132915
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181
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2; Mismatches
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Pred. No.
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ATP (POTENTIAL)
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NON ALPHA-HELICAL,
                                                                                                                Werhahn W.,
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                                                                         mitochondrial proteins
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                                                                                                                Braun H.-P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  covered by 90 Pl, TAC
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Best Local &
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15-SEP-2003
15-SEP-2003
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-Bristol N2;
MORTIMORE B.J.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UDP-glucose + alpha-D-galactose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for conmodified and this statement is not removed. Usage by and for conmodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Probable galactose-1-phosphate uridylyltransferase (BC 2.7.7.12)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Created)
15-SE
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Pfam; PF01459; Euk_porin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Outer membrane.
SIMILARITY: BELONGS TO THE TOM40 FAMILY.
CAUTION: Ref.1 sequence differs from that
                                                                                                                                                                                                                                                                                                                                                               alpha-D-glucose 1-phosphate + UDP-galactose COFACTOR: Binds 1 zinc and 1 iron ion per su
                                                                                                                                                                                                                     SIMILARITY: Belongs to the galactose-1-phosphate uridylyltransferase family 1.
                                                                                                                                                                                                                                                                                                               COFACTOR: Binds 1 zinc and 1 iron ion PATHWAY: Galactose metabolism; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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InterPro; IPR001937, Galp UDPtransf.1.
InterPro; IPR005851; Galp Utransf.C.
InterPro; IPR005850; Galp Utransf.N.
InterPro; IPR005849; Galp Utransf.N.
Pfam; PF01087; Galp UDP transf; 1.
Pfam; PF02744; Galp UDP transf; 1.
Pr0Dom; PD005651; Galp UDP transf; 1.
                                                                                             when by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement or send an email to the statement is not removed.
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Seery L.T., Schoenberg D.R., Barbaux S.,
"Identification of a novel member of the
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Ve. Amphibia; Batrachia; Anura; Mesobatrachia; Xenopodinae; Xenopus.
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                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                Pentraxin PXN1.
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                                                                  EMBL; L19881; AAC38013.1; HSSP; P07629; 1HAS.
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-!- SIMILARITY:
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IPR001759;
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>S00117; GAL_P_UDP_TRANSF_I;
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PENTAXIN FAMILY.
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ia; Pipoidea; Pipidae;
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Pfam; PF00354; pentaxin; 1 PRINTS; PR00895; PENTAXIN. ProDom; PD002153; Pentaxir

SMART; SM00607;

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DR SMART; SM00159; PTX; 1.

DR PROSITE; PS00289; PENTAXIN; 1.

KW Pentaxin; Signal.

FT SIGNAL 1 1 4 POTENTIAL.

FT SIGNAL 1.

FT CHAIN 15 416 PENTRAXIN FUSION PROTEIN.

FT DOMAIN 232 416 PENTRAXIN FUSION PROTEIN.

FT DISULFID 251 311 BY SIMILARITY.

FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 221 221 N-LINKED (GLCNAC. .) (POTENTIAL).

SQ SEQUENCE 416 AA; 47241 MW; GEEDE45E913A2BD7 CRC64;

Query Match

Best Local Similarity 66.7%; Perd. No. 21;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GSIASNYVQ 13

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Db 64 GSLASNYME 72

Search completed: January 12, 2004, 06:59:43

Job time: 11.1094 secs
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_inverteb:
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6: sp_mammal:*
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מחויות איניות מרוים				homo sapi	Q02697 podospora a	O26284 methanobact		ersinia	Q9w4g3 drosophila	Q942el oryza sativ		Q99ie9 human immun	Q97687 human immun	human	Q8j3y0 human immun			Q27536 caenorhabdi		œ	ω	Q91mq0 arabidopsis		r	Q8xks7 clostridium	Q9x331 bacillus an	Q8kyn9 bacillus an	Q8adel human immun

## ALIGNMENTS

B 8	Ма	S E PLUS STEPLES STEPL	RESULT
1 TRSSGSIASNYVQ 13             23 TRSSGSIASNYVQ 35	Query Match 100.0%; Score 62; DB 4; Length 112; Best Local Similarity 100.0%; Pred. No. 0.00022; Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Q96JD1 PRELIMINARY; PRT; 112 AA. Q96JD1, Q96JD1, Q96JD1 (TrEMBLrel. 19, Created) Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update) Q1-DEC-2001 (TrEMBLrel. 23, Last sequence update) Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update) Amyloid lambda 6 light chain variable region PIP (Fragment). HOMO septens (Human) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; [1] SEQUENCE FROM N.A. TISSUE=Bone marrow; Perfecti V., Casarini S., Colli Vignarelli M., Merlini G.; Pamyloid lambda 6 light chain variable region PIP."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. InterPro; IPR003106; Ig_MHC. InterPro; IPR003106; Ig_MHC. InterPro; IPR003106; Ig_MHC. InterPro; IPR003106; Ig_WHC. Pfam; PF00047; ig; l. SMART; SM00406; IG_V; l. PROSITE; PS50835; IG_LIKE; l. NON_TER 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;	TITT 1

RESULT 2

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C QV9J3; Q94879; O18369; Q26297;

T 01-MAY-2000 (TrEMBLrel 13, Created)

T 01-MAY-2000 (TrEMBLrel 13, Last sequence update)

T 01-MAY-2003 (TrEMBLrel 23, Last annotation update)

T 01-MAY-2003 (TrEMBLrel 23, Last annotation update)

T 10-MAY-2003 (TrEMBLrel 23, Last annotation update)

T 10-MAY-2003 (TrEMBLRel 23, Last annotation update)

B Yrosine-protein kinase Src42A (EC 2.7.1.112)

N SRC42A OR SRC41 OR TK5 OR CG7873.

N SRC42A OR SRC41 OR TK5 OR CG7873.

C Neoptera, Endopterygota; Diptera, Brachycera, Muscomo:

C Neoptera, Endopterygota; Diptera, Brachycera, Muscomo:

SRC42A OR SRC41 OR TK5 OR CG7873.
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Best Local
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SEQUENCE
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"Amyloid lambda 6 light chain variable region SAR.";
Submitted (WAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF267875; AAK58887.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig-MHC.
InterPro; IPR003006; Ig-W.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PSS0835; IG-LIKE; 1.
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Q96JDO;
Q1-DDC;
Q1-DBC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Amyloid lambda. 6 light chain variable region SAR
MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxxer E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley;
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                           Takahashi F., Endo S., Kojima T., Saigo K., "Regulation of cell-cell contacts in develog Darc41, a new, close relative of vertebrate Genes Dev. 10:1645-1656(1996).
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116 AA;
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84.6%;
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1; Mismatches
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Pred. No. 0.022;
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;s in developing Dro;
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                              wiklos G.L.G.,
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easley E.M.,
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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Doubin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Halli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., Wcleod M.P., McPherson D.,
RA McHout S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nixon K.A., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang A.H., Wang X.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.M., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RI Silma S. S. 2015 (2000).
RA OATES A.C., Wollberg P., Achen M.G., Wilks A.F.;

RA OATES A.C., Wollberg P., Achen M.G., Wilks A.F.;

RA OATES A.C., Wollberg P., Achen M.G., Wilks A.F.;

RT "Sampling the genomic pool of protein tyrosine kinase genes using the prolymerase chain reaction with genomic DNA,";

RL Biochem. Biophys. Res. Commun. 249:660-667(1998).

RL Biochem. Biophys. Res. Commun. 249:660-667(1998).

RE SIRVITAL FOR CORRECT EYE MORPHOGENESIS (OMMATIDIAL R7 NEURON FORMATION), THIS REQUIRES THE RASI/MAPK SIGNAL TRANSDUCTION CORGANIZATION AND CELL-CELL CONTACTS IN DEVELOPING OMMATIDIA.

CO PATHWAY. MAY BE INVOLVED IN THE REGULATON OF CYTOSKELETON CORGANIZATION AND CELL-CELL CONTACTS IN DEVELOPING OMMATIDIA.

CO PATHWAY. MAY BE INVOLVED IN THE REGULATON OF CYTOSKELETON COMMATIDIA.

CO PATHWAY. AND PHOTORELET OUT OUT TYROSINE = ADP + PROTEIN TYROSINE FROSEIN IS SEEN IN VISCERAL MESODERM, HINDGUT, BRAIN, ANAL PADS CHARLES AND PHOTORECEPTOR PRECURSORS IN THE EYE-ANTENNA DISKS CONTROL TO THE MORPHOGENETIC FUUROW.

CO POSTERIOR TO THE MORPHOGENETIC FUUROW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIINE=92008631; runneu----;
Shishido E., Emori Y., Saigo K.;
Shishido E., Emori Y., Saigo K.;
"Identification of seven novel protein-tyrosine kinase genes
"Identification of seven novel protein-tyrosine kinase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN=BerKeley: TISSUE=Embryo;

STRAIN=BerKeley: TISSUE=Embryo;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Stapleton M., Chavez C., Dorsett V., Farfan D., Frise E., George
Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George
Conzalez M., Guarin H., Li P., Liao G., Mindad A., Mungall C.,

Nunco J., Pacleb J., Pargas V., Park S., Phouanenavong S., Wa
Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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           DUMAIN. BELONGS TO THE SRC SIMILARITY: CONTAINS 1 SH2 SIMILARITY: CONTAINS 1 SH3 L; D42125; BAA07705.1; -.
                                                                                                                                      LARVAE AND PUPAE.
SIMILARITY: TO OTHER PROTEIN-TYROSINE
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                                                                                                                                            THE CATALYTIC
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TISSUE=Bone marrow;
Perfetti V., Casarini S., Colli Vignarelli M., Me:
"Amyloid lambda 6 light chain variable region NEG
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ dat
EMBL; AF267873; AAK58585.1;
InterPro; IPR003006; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity
Matches 9; Conser
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PRINTS; PRO0109; TYRKINASE.

ProDom; PD000001; Prot kinase; 1.

ProDom; PD000003; SH2; 1.

ProDom; PD000066; SH3; 1.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS50011; PROTEIN KINASE DOM; 1.

PROSITE; PS00109; PROTEIN KINASE TYR; 1.

PROSITE; PS00101; SH2; 1.

PROSITE; PS50001; SH3; 1.
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InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Amyloid lambda 6 light chain variable region NEG (Fragment).
Homo sapiens (Human).
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SH3 domain; I
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                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0004603; Src42A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
Ą,
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                                                                                                                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
222
262
276
276
370
376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59069 MW;
11908 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.7%;
75.0%;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No.
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V -> I (IN REF. 4 AND 5).
GNIVKI -> SNVVKM (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH3.
                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1EF196E4D7AE61E9 CRC64;
080B4B37E2360B06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase; ATP-binding; SH2 domain;
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11;
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NEG.";
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RESULT 6
Q8X1V8
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Best Local S
Matches 8
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Best Local Similarity
Matches 10; Conser
     Query Match
Best Local Similarity
                                                                                                STRAIN-ATCC14332;
Oda K., Abe K., Kasahara S., Nakajima T.;
Oda K., Abe K., Kasahara S., Nakajima T.;
Oda K., Abe K., Kasahara S., Nakajima T.;
Cloning and nucleotide sequencing of the exo-be (exgS) from Aspergillus saitoi.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ date (EMBL, AB070739; BAB83607.1; -
InterPro; IPROMO6162; PBOANTETHEINE; 1.
PROSITE; PSO0012; PHOSPHOPANTETHEINE; 1.
PAGURDASE; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O14244;
O1-JUN-1998
O1-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8X1V8;
Q8X1V8;
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
conserved hypothetical protein.
spAc6F6.13C.
Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota
Eurotiales; Trichocomaceae;
NCBI TaxID=186681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Exo-beta-1,3-glucanase (EC 3.2.1.58).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gentles S., Churcher C.M., Barr Submitted (SEP-1997) to the EMB EMBL; Z98981; CAB11736.1; -. GeneDB Spombe; SPAC6F6.13c; -.
                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  Aspergillus saitoi (Aspergillus phoenicis).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. SEQUENCE 778 AA; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          014244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000734; Lipase.
ROSITE; PS00120; LIPASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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                                                                                Glycosidase.
945 AA; 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86129 MW; 0B0B2AC38E5D1796 CRC64
                                                                                99332 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64.5%;
72.7%;
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76.9%;
       62.9%;
77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                           mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB
Pred. No. 45;
                                                                                58D0CC3D84853BC0 CRC64;
       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             778
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DB
89;
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3.2;
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                                                                                                                                                                                                          databases
                                                                                                                                                                                                                                                       beta-1,3-glucanase
                          Length 945;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 778;
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Best Local S
Matches 8
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                                                                                                                                                                                                                                                                                                                                                            Q8MKV0;
01-OCT-2002
01-OCT-2002
01-MAR-2003
CG30004-PA.
MEDLINE=20196006, PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.M., Hoskins R.A., Galle R.F.,
Scheers S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase;
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CON
EMBL; AL353092; CAC
HSSP; P08631; 1AD5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2003
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01-MAR-2001
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                                                                                                                                                                           STRAIN=Berkeley;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit
                                                                                                                                                                                                                                                                                                                                               CG30004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8MKV0
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InterPro; IPR001452;
Pfam; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50002; SH3; 1.
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3 (TrEMBLrel.
(Hemopoietic
                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Primates;
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RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
T "Sequencing of Drosophila melanogaster genome.";
L Submitted (MAR-2000) to the RMBI/General/Content."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W. RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Glodek A., Gong F., Gorrell J.H., Ku Z., Guan P., Harris M.A., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Mang Z., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A., Zheng Y.H., Zhong F.N., Zhong W., Zhou X., Smith H.O RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; Thu X., Smith H.O RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; Thu X., Smith H.O Ra Ground R. Strong E.W., Rubin G.M., Venter J.C.; Thu X., Smith H.O
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T.L., Bergman (
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003
SEQUENCE FROM N.A.
STRAIN=CECT 20197;
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Mansur M., Suarez T
                                                                                                                                                      Trametes sp. I-62.
Eukaryota, Fungi, Basidiom
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Phenoloxidase (EC 1.10.3.2)
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STRAIN=98UC57143;
MEDLINE=22375625; PubMed=12487816;
MEDLINE=22375625; PubMed D., Sewankambo N., Wabwire F., Kim B.,
Harris M.E., Serwadda D., Sewankambo N., Wabwire F., Kim B.,
Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
Kigozi G., Kiwanuka N., Phillips J.B., Meehen M., Lutalo T.,
Lane J.R., Merling R., Gray R., Wawer M., Birx D.L., Robb M.L.,
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"Among 46 Near Full Length HIV Type 1 Genome Sequences from Rakai Pistrict, Uganda, Subtype D and AD Recombinants Predominate.";
AIDS Res. Hum. Retroviruses 18:1281-1290(2002).
EMBL, AF484514; AAN73764.1;
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Virology 278:103-110(2000).
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T., Fernandez-L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FFC0A709464CA6D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lentivirus
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                                                                                                                                                                                                                                                                                                                                                                                                                            ጅ
                                                                                                                                                                                                                                                                                                        update)
  Brizuela M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Merling R., Robb M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
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RESULT 12
Q9XXR3
Q9XXR
ID Q9XXR
AC Q9XXR
DT 01-NC
DT 01-NC
DT 01-MA
DE Y51A2
GN Y51A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
Q9KKL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                            Q9XXR3
Q9XXR3;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9KKL8;
Q9KKL8;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=El TOR N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P.

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a laccase gene family in the basid omycete CECT 20197.";
Appl. Environ. Microbiol. 63:2637-2646(1997).
EMBL; U65399; AAB63443.1; -.
HSSP; P37064; IAOZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                      Pfam; PF03961; DUF342; 1.
Hypothetical protein; Complete
SEQUENCE 556 AA; 60476 MW;
                                                                                                                                                                                                                                                                                                                                                                  Nature 406:477-483(2000).
EMBL; AE004434; AAF96978.1;
TIGR; VCA1085; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00394; Cu-oxidase; 3.
PROSITE; PS00079; MULTICOPPER_OXIDASE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gonzalez
                                                                                                                                                                                                                                                                                                                                                                                                                    "DNA sequence of both chromosomes cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                      interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro;
                                                                                                                                                                         343
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8; Conserv
                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                         RSSGSIASNYVQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSAGSTAYNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.B.;
                                                                                                                                                                         KSGGSIRANYAQ 354
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                                                                                                                                                                                                                                                                                                                                                     IPR005646; DUF342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) (TrEMBLrel. 15, C)
) (TrEMBLrel. 15, Li
? (TrEMBLrel. 22, Li
al protein VCA1085.
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(TrEMBLrel. 2
1 protein VCA)
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61.3%;
72.7%;
                                                                                                                                                                                                                                                       61.3%;
58.3%;
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                               12,
12,
23,
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                             Created)
Last sequence that annoted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 38; DB
Pred. No. 72;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                         Score 38; DE
Pred. No. 77;
                                                                                                                                                                                                                                                                                                 proteome.
8565B105E6F2E2DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD226C498770DDE4 CRC64;
                                                                                                                                                                                                                                          Mismatches
                               sequence update)
annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      of the
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                                                                                              606
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72;
                                                                                                                                                                                                                                                                        В
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                                                                                                                                                                                                                                                                      Length 556;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen Vibrio
                                                                                                                                                                                                                                          Indels
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Y51A2D.4 protein.

SO DE RESERVA DE RESER

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RESULT
Q9V5B0
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
A Manartides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
B Barandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
A Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,
A Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
A Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadeu E., Center A., Chandra I.,
A Gepablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PROULL, TIGRO879; SP; 1.

TIGREAMS; TIGRO879; SP; 1.

PROSITE; PS50850; MFS; 1.

PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.

SUGAR_TRANSPORT. Transport.

SUGAR_TRANSPORT_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Harapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9V5B0;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wormpep; Y51A2D.4; CE19201.
InterPro; IPR007114; MPS.
InterPro; IPR003828; Sub_transporter.
InterPro; IPR003663; Sugar_transpt.
InterPro; IPR003663; Sug_transporter.
Pfam; PF00083; Sug_transporter.
Pfam; PF00081; Sugar_tr; 1.
PRINTS; PR00171; SUGRTRNSPORT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CG1776 protein. CG1776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=99069613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MCMUrray A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9V5B0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL021497; CAA16400.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peloderinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61.3%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13, Created)13, Last sequence update)23, Last annotation update)
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RE Science 287:2185-2195(2000).

RE Semilians S.M., Woodage T., Worley S.R., Wang S., Smith H.O. Finshill R., Shang S., Yao Q., Zheng L., Science 287:2185-2195(2000).
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QBMMT7;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                   Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noege "Sequence and Analysis of Chromosome 2 of Dictyostellum."; Submitted (MAX-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AC117076; AAM33596.1; -. SEQUENCE 1041 AA; 117567 MW; 5204E9AC97RDD777 7777
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Microtubule-associated protein CP224. 6/101. Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium NCBT Travillo.
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PROSITE; PS00108; PROTEIN KINASE_ST; 1.
ATP-binding; Kinase; Serime/threonine-protein kinase; 3E2QUENCE 762 AA; 83776 MW; E447DFEC9AE6E8ED CRC64;
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InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_Ehr_pkinase.
Pfam; PF00069; pkinase; 1.
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HSSP; Q63450; 1A06.
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Search completed: January 12, 2004, 07:02:08 Job time: 31.4062 secs
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Q9H3D8;
01-MAR-2001
01-MAR-2001
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Zhao B., Xu Y.Y., Liu Y.Q., Wang X.Y., Lui B., Ye J., Song L.,
Zhao Y., Cao H.Q., Zhao X.W., Gao Y., Zhang C.L., Zhang J., Liu L.S.,
Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q., Yuan J.G., Liew C.C.,
Zhao M.S., Hui R.T.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF719814; AAG47945.1; -.
InterPro; IPR007087; Znf C2H2.
SMART; SM00355; ZnF C2H2; -1.
PROSITE; PS00028; ZINC FINGER_C2H2_1; 1.
SMART; SM00355; ZnF C2H2; -1.
                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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AAR23777	AAR23771	AAR23769	AAR23826	AAR23822	AAR23776	AAR41722	AAR23823	AAR23821	AAR23817	AAR23779	AAR23775	AAR23740	AAR23814	AAR23778	AAR23772	AAY68807	ABG31476	ABG31465	AAY68804	AAR50108	AAR23736	ABB57957	ABG95659	ABG07372	ABP56512	ABP56511	AAW14785	88	AAW16590	85	ABP45520	ABP45364	ABP45156	11	ABP44898
Recombinant light	Recombinant light			Recombinant light		Aglycosylated anti	light	Recombinant light	Recombinant light	Recombinant light	Recombinant light	Recombinant light	Recombinant light		Recombinant light	A light chain vari	Light chain variab	Rat immunoglobulin	Amino acid sequenc	CDR (d). Syntheti	CDR (d) . s	Drosophila melanog	Human nucleic acid	diagn	Human anti-Fc-epsi	Human anti-Fc-epsi	monoc		Anti-RSV F glycopr	ס	BLyS	BLyS	BLyS	BLyS	Human BLyS binding

## ALIGNMENTS

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RESULT 1
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TANGER REPORT OF THE PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; antibody; scFv; CDR; complementarity determining region; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; heromostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke; ischaemia; cardiovascular disease; immunological disease; liver disorder;
                                                                                                                                           30-JUN-1999; 99US-0345468.
06-DEC-1999; 99US-0454824.
14-PEB-2000; 2000US-0503387.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W0200100810-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-TANGO 268 scFv CDR, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB61296;
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                                           (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                             30-JUN-2000; 2000WO-US18152.
                                                                                                                                                                                                 99US-0345468.
99US-0454824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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RRSULT 2
ABULI 3X
ABULI 2X
ABULI ABULI
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ABULI
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Gegg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein vI (GPVI), also called TANGO 268. The GPVI polynucleotides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with abstrant expression or activity of CGPVI. These disorders include bleeding disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders preferably they are used to prevent acture cardiac ischaemia following angioplasty and metastatic cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboembolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; cardiovascular disease; angina pectoris; myocardial infarction; coronary restenosis; atherosclerosis; immunological disorder; developmental disorder; embryonic disorder; liver disorder; developmental disorder; embryonic disorder; liver disorder; cerebral vascular disease; venous thromboembolism disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, tr and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Busfield SJ, Ville Qian MD, Kingsbury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                           09-APR-2001; 2001US-0829495.
                                                                                                                                                         09-APR-2002; 2002WO-US11122
                                                                                                                                                                                                                                                                                     WO200280968-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU11262 standard; Peptide; 13
                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Similarity 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRSSGSIASNYVQ 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 VLCDR1 Peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ູດ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jandrot-Perrus M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ₿
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Busfield SJ, Villev
Qian DM, Kingsbury
             Villeval
             'n
             Jandrot-Perrus M,
             Vainchencker
             ξ.
              Gill DS;
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Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis

Claim 10; Page 111; 236pp; English

CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or CC block TANGO 268 binding to extracellular matrix components, or as a CC Collagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration, CC morphology, differentiation and/or function of megakaryocytes and plateletes, including during development e.g. embryogenesis, modulating plateletes, including during development e.g. embryogenesis associated degramulation. They are also useful for modulating platelet aggregation and CC inflammation and/or thrombosis, and modulating disorders associated with abnormal or aberrant megakaryocyte and/or platelet proliferation, migration, morphology, differentiation and/or function, e.g. bleeding CC disorders such as thrombocytopaenia. Other diseases which may be condulated by these antibodies are thrombotic disorders, cerebral CC vascular diseases including angina pectoris, generation, pain and ulceration, currently componently causes including angina pectoris, myocardial infarction, coronary crestenosis, atheroscalerosis, etc); immunological disorders, cerebral CC vascular diseases, venous thromboembolism diseases invention, coronary crestenosis, atheroscalerosis, etc); immunological disorders, cerebral CC vascular diseases, venous thromboembolism diseases, coronary diseases, cerebral coronary diseases, cer variable heavy (VH) complementarity determining region (CDR)1, or VH CDR3; or VH CDR3; or VH CDR3, a generate the This invention antibodies of the invention. relates to a novel purified antibody comprising £a CDR2

Sequence 13 AA;

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Query Match
Best Local S
Matches 13
                13;
1 TRSSGSIASNYVQ 13
                       Similarity
                Conservative
                       100.0%;
                0
                        Score 62;
Pred. No.
                 Mismatches
                       6.3e-05;
                                 DB 24;
                 0
                                Length
                 Indels
                                 13;
                 0,
                 Gaps
                 0
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RESULT 3
ABP56510
ABP56510 standard;
 Protein;
 98
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밁 S

TRSSGSIASNYVQ 13

Human anti-Fc-epsilon-R1 alpha autoantibody light chain V1-22

20-MAR-2003

(first

entry)

Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive; allergic disease; urticaria; late phase allergic reaction; malignanc intrinsic asthma; drug intolerance; food intolerance; immunoglobulin conditional autoimmunity; IgE mediated disease. immunoglobulin E;

Homo sapiens

Synthetic

WO200282085-A2

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RESULT 4
AAO18434
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor alpha-chain and an autoantibody against its alpha-chain. Also described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain for identifying and obtaining an inhibitor of a pathological process; (2) use of the identified inhibitor for inhibiting activity of the autoantibody against the Fc-epsilon-R1 receptor alpha-chain; and (3) a compound identified by the method, which binds but does not activate the receptor; and (4) a polypeptide capable of specific binding to the Fc-epsilon-R1 receptor alpha-chain. The method is useful for
                                                                                                                                                                                                                                                                                                                      AAO18434 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtaining an inhibitor of a pathological process e.g. imbalance between cell-bound and free IgE e.g. allergic disease (urticaria, late phase allergic reactions, intrinsic asthma, drug intolerance and food intolerance), IgE mediated disease or malignancy. The compound is useful for treating a pathological process, particularly conditional autoimmunity. The present sequence represents a human recombinant anti-FC-epsilon-Rl alpha autoantibody light chain protein sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method for identifying and obtaining an inhibitor of a pathological process. The method comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor alpha-chain and an autoantibody against its alpha-chain. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoantibody against its alpha-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying and obtaining inhibitor of a pathological process for treating e.g. autoimmunity comprises determining if a compound is capable of modulating the binding of the Fc-epsilon-R1 receptor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Miescher
                                                                                           DE10059930-A1
                                                                                                                                            Homo sapiens
                                                                                                                                                                           melanoma;
                                                                                                                                                                                                                       Anti-GD2 antibody light chain #11.
                                                                                                                                                                                                                                                          11-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-APR-2001; 2001US-281024P
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23-NOV-2000; 2000DE-1059930
                              23-NOV-2000; 2000DE-1059930
                                                                                                                                                                                            Anti-GD2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZLB BIOPLASMA AG
                                                                                                                                                                                          antibody;
                                                                                                                                                                                                                                                                                                                                                                                                    TRSSGSIASNYVO 35
                                                                                                                                                                                                                                                                                                                                                                                                                        TRSSGSIASNYVQ 13
                                                                                                                                                                          vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; 29pp; English.
                                                                                                                                                                                                                                                                                                                      protein; 110
                                                                                                                                                                        neuroectodermal tumour; cancer; neuroblastoma; gene therapy; cytostatic; disialoganglioside (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                      A
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. 0.00065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                           GD2.
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RESULT 5
AAU02522
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprises human antibody antibodies -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a composition for treating tumours positive for distaloganglioside GD2 which is based on human antibody fragments that activate the immune system against GD2, specifically inducing anti-GD2 antibodies. The composition can be used in the treatment of neuroblastoma and melanoma. The present sequence is an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                           Claim 1;
                                                                             Panel of specific binding members of antibody molecules which bind whole adipocytes is used in the treatment of obesity and obesity related diseases -
                                                                                                                         N-PSDB;
                                                                                                                                                        Edwards BM, Main SH,
                                                                                                                                                                                                  12-OCT-1999;
                                                                                                                                                                                                                      11-OCT-2000; 2000WO-GB03900
                                                                                                                                                                                                                                          19-APR-2001.
                                                                                                                                                                                                                                                             WO200127279-A1
                                                                                                                                                                                                                                                                                                                                       Anti-adipocyte monoclonal antibody light chain, FAT 13.
                                                                                                                                                                                                                                                                                                                                                                                                     AAU02522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anti-GD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Fig 7A; 14pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-510006/55
                                                                                                                                                                                                                                                                                                                 Antibody; adipocyte; heavy chain; light chain; obesity;
                                                                                                                                                                             (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                         2001-282031/29.
)B; AAS03422.
                                                                                                                                                                                                                                                                                                        disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TRSSGSIASNYVQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISCHER P.
UTTENREUTHER-FISCHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody light chain.
                                                          Page 106; 182pp;
                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRSSGSTASNYVQ 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                  99US-0158812.
                                                                                                                                                                                                                                                                                                       complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        German
                                                                                                                                                       Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumors that produce disialoganglioside fragment able to induce anti-idiotypic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krueger
                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 23;
Pred. No. 0.00074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                        region;
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AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid sequences of anti-adipocyte monoclonal antibody heavy chain, light chain, and heavy chain complementarity determining regions (CDR) of the invention. The antibodies can be used in the treatment of obesity and obesity related diseases. The antibodies can be used to deliver drugs or

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RESULT 6
AAG76011
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Best Local S
Matches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pro-drugs directly to the fat mass of an obese patient or the antibody can be used as a therapeutic itself. Antibodies binding specifically to adipocytes can be used to activate the immune system to destroy the cells by complement mediated lysis. The antibodies may be labeled with a detectable label such as radiolabel, fluorescent or chemical group and used in methods of diagnosis in human subjects e.g. to determine the presence of adipocyte antigen on the surface of an adipocyte to detect or determine the presence or level of adipocytes in a cell or tissue sample. The antibodies can be used as an alternative means of treatment for obese patients other than undergoing surgery to remove excess fat. Antibodies for different types of fat deposits can also be produced e.g. intrabdominal fat associated with heart disease.
cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis
                                                                                                                                                                                                                                                                                           AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), wher the proteins are collectively known as colon cancer antigens. The c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-235357/24.
N-PSDB; AAH35416.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG76011 standard; Protein; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 8234-8235; 9803pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-SEP-2000; 2000WO-US26524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              colorectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acids encoding 4277 human for preventing, diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRSSGSIASNYVQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein SEQ ID NO:6775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E,
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              colon cancer-associated polypeptides, and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
0.00077;
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                                                                                                                                                                                                                                                                                           The colon
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RESULT 7
ABJ19832
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      amino acid sequence selected from at least one, two or three CDR region(s) of a VH or VL domain where the first antibody immunospecifically inhibits a VEGF-2 polypeptide. The isolated polymucleotide is useful in diagnosing, treating, preventing, prognosing, ameliorating or monitoring diseases associated with aberrant VEGF-2 or VEGF-2 receptor expression or lack of VEGF-2 or VEGF-2 receptor function, such as cancer and other proliferative disorders, cardiovascular disorders (arrhythmias), cerebrovascular disorders (e.g. cerebral disorders).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention.

No. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                              New isolated polynucleotide encoding an antibody which inhibits VEGF-2 polypeptide, useful for diagnosing, treating or preventing diseases associated with aberrant VEGF-2 expression or function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cerebrovascular disorder; cerebral anoxia; inflammatory disease; infectious disease; autoimmune disease; rheumatoid arthritis; Systemic Lupus Erythematosus; allergy; diabetic retinopathy; psoriasis; angiogenesis; wound healing; vascular tissue repair; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiarthritic; antidiabetic; ophthalmological; antiallergic; immunosuppressive; dermatological; antipsoriatic; vulnerary; antil CDR region; VH domain; VL domain; immunospecific; VEGF-2; cancer; proliferative disorder; cardiovascular disorder; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  13-APR-2001; 2001US-283385P.
24-JAN-2002; 2002US-350366P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human VEGF-2 related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and treatment of colorectal carcinomas and cancers. AAH37196 and AAB77789 represent sequences used in the exemplification
                                                                                                                                            The invention relates to an isolated polynucleotide encoding a first antibody at least 95-100% identical to a second antibody comprising
                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                cancer or
                                                                                                                                                                                                                                                                                                                   WPI; 2003-092991/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200283704-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        АВJ19832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-APR-2002; 2002WO-US11474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRSSGSIASNYVQ 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRSSGSTASNYVQ 56
                                                                                                                                                                                                                                inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           161 AA;
                                                                                                                                                                                               Page 389-390; 425pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiant; cardiovascular; antiinflammatory; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
| llarity 100.0%;
| Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                      ×SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are present for
                                                                                                                                                                                                                                                   preventing function,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
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of the
                                                                                                                                                                  a first
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   diseases
                                                                                                                                                                                                                                                   e.g.
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diseases,

infectious

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                                                             Query Match
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Matches 12
                                                                                                                                                         diabetic retinopathy or psoriasis. The polynucleotide, polypeptide and antibodies may also be used to stimulate angiogenesis, wound healing, and promoting vascular tissue repair. The polynucleotide and polypeptide may also be used for in vitro purposes related to scientific research, synthesis of DNA and manufacture of DNA vectors, and for the production of diagnostics and therapeutics to treat human diseases. This sequence represents a human VEGF-2 related protein of the invention.
                                                                                                                                                                                                                                                           (e.g. rhe diabetic
                                                                                                                              Sequence
160 TRSGGSIASNYVQ 172
                                                                                                                                                                                                                                                                          rheumatoid arthritis, Systemic Lupus Erythematosus, allergies),
                               μ
                                                                              Similarity
                         TRSSGSIASNYVQ
                                                                                                                              248
                                                               Conservative
                                                                                                                              AA;
                                                                              93.5%;
                               13
                                                                              Score
Pred.
                                                               Mismatches
                                                                              No.
                                                                                0.011;
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                                                                                             24;
                                                                                           Length 248;
                                                               Indels
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ABP45223
                                                                                                                        ABP45223 standard;
                                                                               WO200202641-A1
                                                                                                          Human
                                                                                                                   ABP45223
                                                                                                              19-AUG-2002
                                                                          10-JAN-2002
                                                                                                                             œ
                                                                                    sapiens.
                                                                                                         BLyS binding scrv SEQ ID 1234.
                                                                                                              (first entry)
                                                                                                                        Protein;
                                                                                                                        258
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BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomoullatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2001; 2001WO-US19110
2002-114799/15
                                                       ,MS
                                                                                                                  CAMBRIDGE
                                                                                                                                              HUMAN GENOME
                                                    Barash SC,
                                                                                                               ANTIBODY TECHNOLOGY:
                                                                                                                                              SCI
                                                    Choi GH,
                                                                                                                                                 INC
                                                    Vaughan T,
                                                    Hilbert D;
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Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
Autoantibody; Fc-epsilon-R1 receptor alpha-chain; immunosuppressive; allergic disease; urticaria; late phase allergic reaction; mallgnancy; intrinsic asthma; drug intolerance; food intolerance; immunoglobulin E; conditional autoimmunity; IgE mediated disease.
                                                                                             Human anti-Fc-epsilon-R1 alpha autoantibody light chain UG-alpha-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                  20-MAR-2003
                                                                                                                                                                       ABP56513;
                                                                                                                                                                                                          ABP56513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           administered to treat diseases associated with aberrant BLyS
                                                                                                                                                                                                                                                                                                          170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                           TRSSGSIASNYVQ 13
                                                                                                                                                                                                                                                                                                        TRSSGSIDSNYVQ 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                (first entry)
                                                                                                                                                                                                          Protein; 112 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                  д 23;
0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
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Gaps

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RESULT 9
ABP56513
ID ABP5
XX A
                      CC The present invention describes a method for identifying and obtaining CC an inhibitor of a pathological process. The method comprises determining CC if a compound is capable of modulating the binding of the Fc-epsilon-R1 CC receptor alpha-chain and an autoantibody against the Fc-epsilon-R1 receptor CC described: (1) use of the autoantibody against the Fc-epsilon-R1 receptor CC alpha-chain for identifying and obtaining an inhibitor of a pathological CC process; (2) use of the identified inhibitor for inhibiting activity of CC the autoantibody against the Fc-epsilon-R1 receptor alpha-chain, and CC (3) a compound identified by the method, which binds but does not CC activate the receptor; and (4) a polypeptide capable of specific binding CC to the Fc-epsilon-R1 receptor alpha-chain. The method is useful for CC obtaining an inhibitor of a pathological process e.g. imbalance between CC cell-bound and free IgE e.g. allergic disease (urticaria, late phase CC allergic reactions, intrinsic asthma, drug intolerance and food CC infolerance) TCF madiater disease contains the contains of the contains of the contains the contains of the contains the contai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying and obtaining inhibitor of a pathological process for treating e.g. autoimmunity comprises determining if a compound is capable of modulating the binding of the FC-epsilon-R1 receptor an autoantibody against its alpha-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZLBB-) ZLB BIOPLASMA AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Page 22; 29pp; English.
     IgE mediated disease or malignancy.
The compound is useful
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be

Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -

Page 1874-1875; 3148pp; English.

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RESULT 10
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                                        cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression
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17-OCT-2000; 2000US-240816F.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficies systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for treating a pathological process, particularly conditional autoimmunity. The present sequence represents a human recombinant anti-Fc-epsilon-R1 alpha autoantibody light chain protein sequence the present invention.
                                                                                                                                                 This invention describes novel antibodies that immunospecifically bind (B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The introdies of the invention have
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RESULT 11
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      밁
This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TNP) super family and induces B cell collection and differentiation. The antibodies of the invention have CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory, CC antirheumatic and antiALDS activity and can be used in vaccines to CC inhibit the expression and activity of BLyS. The antibodies bind to BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC biological samples and may be used in this way to diagnose disease CC associated with aberrant expression of BLyS. They may also be CC and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatodi arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
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                                                                                                       This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases as concer, immune, and autoimmune disorders and diseases as concer, immune, and autoimmune disorders and diseases as concer, immune, and autoimmune disorders and concerns the content of a province of the properties.
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diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (c.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP41990-ABP47228 repthe antibodies and fragments of the antibodies described in the me
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17-OCT-2000; 2000US-240816P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 1795-1796; 3148pp; English.
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2001US-277379P.
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Pred. No.
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                                                            (CVID) and
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RESULT 13
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Best Local &
Matches 11
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
                                           cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
acquired immunodeficiency syndrome (AIDS)). ABI the antibodies and fragments of the antibodies of the invention.
                                                                                                                                                                                                    This invention describes novel antibodies that immunospecifically bind of B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; anticheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                       Claim 1;
                                                                                                                                                                                                                                                                                                                   Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-114799/15
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common variable
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                                                                                                                                                                                                                                                                                       Page 2043-2044; 3148pp;
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; 2000US-240816P.
; 2001US-276248P.
; 2001US-277379P.
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Pred. No. 0.09
1; Mismatches
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                                                                                                                                                                                                                                                                                       English
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                               ABP43990-ABP47228 represent
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Best Local S
Matches 11
                                                                                 This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity and super antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases.
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17-OCT-2000; 2000US-740816P
16-MAR-2001; 2001US-276248P
21-MAR-2001; 2001US-277379P
25-MAY-2001; 2001US-293499P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
                                         diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
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                            antibodies and
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CAMBRIDGE ANTIBODY TECHNOLOGY.
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                            fragments of the antibodies described in the method
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Pred. No. 0.095;
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                                                                                                                                                                                                                                                                                                                         g polypeptides, useful for immune disorders -
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RESULT 15
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                                                administering to a mammalian subject a composition comprising the prote (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II). (II) and (III) are useful for diagnostic evaluation of disorders. (I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound heali and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.

Note: The sequence data for this patent did not form part of the printe specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification, but was obtained in electronic format directly from WIPC specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tang YT,
Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair tissue repair central nervous system disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                           The invention relates to an isolated polynucleotide (I) comprising one 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
                                                                                                                                                                                                                                                                                                                     Claim
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                                  ftp.wipo.int/pub/published_pct_sequences
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diabetes and allergies -
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Query Match Best Local S Matches 11

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Search completed: January 12, 2004, 06:58:56 Job time: 33.4844 secs

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Result
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1: /cgn2_6/ptodata/1/pubpaa/USO7

2: /cgn2_6/ptodata/1/pubpaa/USO7

3: /cgn2_6/ptodata/1/pubpaa/USO7
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/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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     US-09-829-495-64
US-10-308-817-117
US-10-269-805-52
US-10-166-698-6785
US-10-109-805-748-1234
US-09-880-748-1234
US-09-972-656-3
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US-09-880-748-125
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Sequence 64, Appl
Sequence 17, Appl
Sequence 117, Appl
Sequence 50, Appl
Sequence 52, Appl
Sequence 6785, Appl
Sequence 42, Appl
Sequence 1234, Appl
Sequence 1234, Appl
Sequence 108, Appl
Sequence 108, Appl
Sequence 90, Appl
Sequence 90, Appl
Sequence 90, Appl
Sequence 1125, Appl
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	18, 7	Sequence 131, App	e 49,	e 49,	Sequence 3, Appli	e 561	e 40	e 91	e 23	66	31	17	e 17	<b>,</b>	e 19	15	e 15,	e 4,	Sequence 8, Appli	e 103	е 9,	ው	e 88,	e 13	Sequence 1, Appli	e 58	e 15:	e 13	Sequence 1167, Ap

## ALIGNMENTS

RESULT 1 US-09-832-312-64

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RESULT 2
US-09-829-495-64
; Sequence 64, Application US/09829495
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CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/35,468
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR PILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                   Query Match 100.0%; Score 62; DB 9; 1
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 13; Conservative 0; Mismatches 0;
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SEQ ID NO 64
LENGTH: 13
TYPE: PRT
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TITLE OF INVENTION: GLYCOPROTEIN VI AND USES
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Publication No. US20040001826A1

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                                                                                                                                                                                                                                                                                                          ; ORGANISM: human US-10-308-817-117
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US-09-829-495-64
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PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: 09/345,468
                                                 GENERAL INFORMATION:
                                                                 Sequence 50, Application US/10269805 Publication No. US20030124129A1
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Best Local :
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SEQ ID NO 117
LENGTH: 98
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Publication No. US20030219861A1
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APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC
FILE REFERENCE: A-722
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/829,495
CURRENT FILING DATE: 2001-04-09
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APPLICANT: Villeval J
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Pred. No. 0.00013;
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; ORGANISM: Homo sapiens
US-10-269-805-52
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SEQ ID NO 50
LENGTH: 110
                                                                        NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.
SEQ ID NO 6785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.1 SEQ ID NO 52
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Best Local Similarity
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Best Local Similarity
                                                                                                                              APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005p1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR PHILING DATE: 1999-08
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR PHILING DATE: 1999-09-29
PRIOR PHILING DATE: 1999-01-29
PRIOR PHILING DATE: 1999-11-03
PRIOR FILING DATE: 1999-11-03
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: OLINER, JONATHAN D.
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
FILE REFERENCE: A-722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/269,805
CURRENT FILING DATE: 2002-10-10
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PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
                TYPE: PRT
ORGANISM: Homo sapiens
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FEATURE:
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                                                        ENGTH: 161
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ilarity 100.0%;
Conservative (
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Pred. No. 0.0013;
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                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 78
LENGTH: 248
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LENGTH: 110
                                                                               Query Match
Best Local
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Publication No.
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Best Local Similarity
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Best Local Similarity
                                                                 Matches
                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
-10-120-414-78
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/328,604
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/120,414
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/283,385
PRIOR FILING DATE: 2001-04-13
                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/350,366
PRIOR FILING DATE: 2002-01-24
NUMBER OF SEQ ID NOS: 85
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TITLE OF INVENTION: Vascular Endothelial Growth Factor-2
FILE REFERENCE: PF112P9
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TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS
FILE REFERENCE: A-722
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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160 TRSGGSIASNYVQ 172
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                                                                                 Similarity
                             TRSSGSIASNYVQ 13
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No. US20030175274A1
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No. US20030124129A1
                                                              Conservative
                                                                             93.5%;
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                                                              Score 58; DB
Pred. No. 0.01
0; Mismatches
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Pred. No. 0.0019;
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                                                                             DB 12; Length 248; 0.016;
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US-09-972-656-108
; Sequence 108, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
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US-09-880-748-1234
                                                                                                         RESULT 11
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US-09-972-656-2
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US-09-880-748-1234
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CÜRRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
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SEQ ID NO 1234
LENGTH: 258
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Best Local Similarity
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Best Local
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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APPLICANT: Tsai, Mei-Mei
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ORGANISM:
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PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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CURRENT FILING DATE: 2001-06-15
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les 12; Conserv
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92.3%;
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; ORGANISM: Homo sapiens
US-09-972-656-108
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; ORGANISM: Homo sapiens
US-09-972-656-3
                                    US-09-972-656-90
                                                                                    GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 90
LENGTH: DET
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CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 108
LENGTH: 216
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SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 3
LENGTH: 13
                                                                                                                                                                                                                                                                                                                        Sequence 90, Application US/09972656
Publication No. US20030099647A1
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Best Local Similarity
Matches 12; Conserva
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
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TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
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APPLICANT: Tsai, Mei-Mei
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                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 TGSSGSIASNYVQ 35
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92.3%;
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92.3%;
87.1%;
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Pred. No. 0.
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Pred. No. 0.048;
Score 54;
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DB 11;
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Length 216;
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Query Match

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US-09-880-748-909
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
; ORGANISM: Homo sapiens
US-09-880-748-1125
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LENGTH: 253
TYPE: PRT
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Matches
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                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1125
LENCTH: 263
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1125, Application US/09880748 Publication No. US20030059937A1
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                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-06-15
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                        NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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5. US20030059937A1
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Pred. No.
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Search completed: January 12, 2004, 07:19:56 Job time : 28 secs	Db 164 TRSSGNIASKYVQ 176	Qy 1 TRSSGSIASNYVQ 13	Hest Local Similarity 84.6%; Pred. No. 0.13; Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Query Match 85.5%; Score 53; DB 11; Length 253;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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        protein search, using sw model
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1: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/JUS06 NEW PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/JUS06 NEW PUB.pep:*

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9: /cgn2_6/ptodata/1/pubpaa/JUS08 PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/JUS09 PUBCOMB.pep:*

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13: /cgn2_6/ptodata/1/pubpaa/JUS10 PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/JUS10 PUBCOMB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/JUS10 PUBCOMB.pep:*
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Match
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Gapop 10.0 , Gapext 0.5
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100.755 Million cell updates/sec
      747907 seqs, 201509753 residues
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      118
120
134
241
247
247
251
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2 US-10-173-551-16

2 US-10-208-817-55

2 US-10-029-9888-85

2 US-10-032-0378-85

2 US-10-032-423A-85

5 US-10-194-975-15

5 US-10-194-975-15

1 US-09-995-529-14

1 US-09-9811-737-3
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Sequence 62, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 1470, Ap
Sequence 48, Appl
Sequence 48, Appl
Sequence 1899, Ap
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Query Matches Matches Qy Db	RESULT 1 US-09-832-312 Sequence 62 Patent No. GENERAL INF APPLICANT: FILE REFER CURRENT FI PRIOR APPL PRIOR FILL PRIOR PILL PRIOR PILL PRIOR APPL PRIOR AP	11111111111111111111111111111111111111
Match 100.0 Local Similarity 100.0 Local Simi	112-62 12 Applica 12 Applica 12 Applica 13 Applica 17 Busfield 17 INVENTION 18 APPLICATION 18 INVENTION 19 APPLICATION 10 APPLICATION 10 APPLICATION 11 APPLICATION 12 APPLICATION 12 APPLICATION 12 APPLICATION 13 APPLICATION 14 APPLICATION 15 APPLICATION 16 APPLICATION 16 APPLICATION 17 APPLICATION 17 APPLICATION 17 APPLICATION 17 APPLICATION 18 APPLICATION	82 92.1 82 92.1 82 92.1 82 92.1 82 92.1 75 84.3 75 84.3 75 84.3 75 84.3 77 83.1 77 84.3 77 83.1 77 84.3 77 83.1 77 84.3 77 75.3 82.0 66 74.2 66 74.2 66 74.2 67 73.0 68 73.0 69 73.0
<pre>%; Score 89; DB 9; %; Pred. No. 8.4e-0 0; Mismatches 17</pre>	09832312 09832312 09832312 05TEIN VI AND USES 0540,0118 064-09 9610,118 09503,387 14 97454,824 96464 97454,824 97454,824 97454,824 97454,824 97454,824 97454,824	253 11 US-09-880-748-1003 253 11 US-09-880-748-1007 262 9 US-09-811-737-19 312 12 US-10-288-917-10 312 14 US-10-052-798-10 312 14 US-09-877-797A-98 250 11 US-09-880-748-1319 250 11 US-09-880-748-1350 17 11 US-09-880-748-1350 17 11 US-09-880-748-1350 17 11 US-09-880-748-1350 17 11 US-09-880-748-1817 249 11 US-09-880-748-1817 249 11 US-09-880-748-1817 249 11 US-09-880-748-1817 241 11 US-09-880-748-1912 251 11 US-09-880-748-2057 243 11 US-09-880-748-2057 244 11 US-09-880-748-2057 248 11 US-09-880-748-914 249 11 US-09-880-748-914 240 11 US-09-880-748-914 241 11 US-09-880-748-914 242 11 US-09-880-748-914 243 11 US-09-880-748-914 244 11 US-09-880-748-914 245 11 US-09-880-748-914 246 11 US-09-880-748-914 247 11 US-09-880-748-914 248 11 US-09-880-748-914 249 11 US-09-880-748-1323 249 11 US-09-880-748-1323
Length 17; 8; 0; Indels 0; Gaps 0;	THEREOF	sequence 1003, Ap sequence 19, Appl sequence 19, Appl sequence 10, Appl sequence 110, Appl sequence 1311, Ap sequence 1311, Ap sequence 11511, Ap sequence 1151, Ap sequence 1150, Ap sequence 1150, Ap sequence 1150, Ap sequence 1170, Ap sequence 1817, Ap sequence 1817, Ap sequence 1817, Ap sequence 1817, Ap sequence 1925, Ap sequence 1932, Ap sequence 1932, Ap sequence 2051, Ap sequence 2053, Ap sequence 1114, Ap sequence 1323, Ap

RESULT 2 US-09-829-495-62 ; Sequence 62, Application US/09829495

Publication No. US20040001826Al

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RESULT 4
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US-09-829-495-62
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US-10-173-551-16
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CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR APPLICATION NUMBER: 09/345,468
PRIOR APPLICATION NUMBER: 09/345,468
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Best Local Similarity
Matches 17; Conserv
Sequence 55, Application US/10308817
Publication No. US20030219861A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lu. Chafen
TITLE OF INVENTION: Antibodies that bind alphaE Integrin
FILE REFERENCE: 1855.2025-000
CURRENT APPLICATION NUMBER: US/10/173,551
CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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Best Local S
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APPLICANT: Villeval J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: GLYCOPROTEIN VI AND USES FILE REFERENCE: 7853-234
                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Local Similarity 88.2%;
hes 15; Conservative
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Pred. No. 1.1e-06;
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Pred. No. 8.4e-08;
): Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/032,037B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FABTSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 98
TYPE: PRT
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US-10-308-817-55
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                                                                          US-10-032-037B-85
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APPLICANT: Bio-Technology General Corp.

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING:

TITLE OF INVENTION: MOISTIES, ANTIBODIES TO SUCH EPITOPES, AND USES THERE

TILE REFERENCE: 10793/46

CURRENT PAPLICATION NUMBER: US/10/029,988B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 204

SOCTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 85

LENGTH: 98
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CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
SEQ ID NO 55
LENGTH: 98
TYPE: PRT
 Query Match
Best Local S
Matches 15
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Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
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Best Local (
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                                                                                         ORGANISM: Homo sapiens
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15; Conserv
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1; Mismatches
Score 82; DB 12;
Pred. No. 7.6e-06;
1; Mismatches 1
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Pred. No.
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                                                                                                                                    US-10-173-551-14
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CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/200
PRIOR FILING DATE: 12/29/200
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 98
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                                                                     Sequence 14, Application US/10173551
Publication No. US20030232387A1
GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
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TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
APPLICANT: Lu, Chafen
TITLE OF INVENTION: Antibodies that bind alphaE Integrin
FILE REFERENCE: 1855.2025-000
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ORGANISM: Homo sapiens
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No. US20040002450A1
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88.2%;
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Pred. No. 7
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; OTHER INFORMATION: CDR3
US-10-173-551-14
                                                                                                RESULT 11
US-09-811-737-3
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US-09-995-529-8
Sequence 3, Application US/09811737
Patent No. US20020099180A1
GENERAL INFORMATION:
APPLICANT: Boehringer Ingelheim Pharma KG
TITLE OF INVENTION: Human FAP-alpha-specific antibodies
FILE REFERENCE: 1-1129
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 120
TYPE: PRT
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Publication No. US20030099655A1
GENERAL INFORMATION:
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Matches
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LENGTH: 118
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Best Local Similarity
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APPLICANT: Tang, Ying
TITLE OF INVENTION: Humanized Collagen Antibodies and
TITLE OF INVENTION: Related Methods
FILE REFERENCE: P-IX 4976
CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
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CURRENT FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSEQ for Windows Version 4.0
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NAME/KEY: SITE
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OTHER INFORMATION: CDR2
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Pred. No. 9.
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CURRENT APPLICATION NUMBER: US/09/811,737 CURRENT FILING DATE: 2001-03-19 NUMBER OF SEQ ID NOS: 32

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-811-737-3
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US-09-880-748-1889
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR PRIOR PRIOR OF THE PRIOR PR
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                                                                                                              FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1470, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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SEQ ID NO 1889
LENGTH: 241
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Best Local Similarity
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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    APPLICATION NUMBER: 60/293,499 FILING DATE: 2001-05-25
                                                                                          FILING DATE: 2001-03-21
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88.2%;
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Pred. No. 1.1e-05;
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Pred. No. 2e-05;
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/2140,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
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FILING DATE: 2001-03-16

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US-10-322-673-48
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US-09-880-748-1470
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/369,877
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR FILING DATE: 2002-06-04
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
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                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 72

SEQ ID NO 48

SED ID NO 48

SERVIT: 247

TYPE: PRT

ORGANISM: Artificial sequence
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SEQ ID NO 1470
LENGTH: 247
TYPE: PRT
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Best Local Similarity
Matches 15; Conserv
                                                                                               Query Match 92.1%; Score 82; DB 12; Best Local Similarity 88.2%; Pred. No. 2.1e-05;
                                                                                  Matches
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PRIOR APPLICATION NUMBER: 60/425,737
PRIOR FILING DATE: 2002-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/322,673
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Salcedo et al.
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/403,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: PF585
                                                                                                                                                                                    OTHER INFORMATION: CM013F04 scFv
                                                                                                                                                                                                   FEATURE:
50 NIKODGSEKYYVDSVKG 66
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                               1 NIKQDGSEKYYADSVRG 17
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No. US20030180296A1
                                                                                Conservative
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88.2%; Pred. No. 2.
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Listing first 45 summaries
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US-09-942-45-37
US-08-545-809A-95
US-08-08-318-1578-23
US-08-08-208-886C-87
US-08-704-744-85
US-08-704-744-85
US-08-704-744-85
US-08-704-744-85
US-08-767-128-2
US-08-318-1578-11
US-08-318-1578-13
US-08-318-1578-17
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13, Appl
14, Appl
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ALIGNMENTS	US-09-277-665-10	US-09-589-927-10	US-09-589-987-12	US-09-589-987-2	US-09-277-665-12	US-09-277-665-2	US-09-589-927-12	US-09-589-927-2	US-09-589-987-4	US-09-277-665-4	US-09-589-927-4	US-08-465-473B-11	US-08-235-838-11	US-09-439-897-4	US-09-167-364-25	US-08-399-889-25	US-09-512-563C-46	US-08-767-128-6
	Sequence 10, Appl	Sequence 10, Appl	Sequence 12, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 4, Appli	Sequence 25, Appl	Sequence 25, Appl	Sequence 46, Appl	Sequence 6, Appli

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pRIOR APPLICATION NUMBER: 09/610,118
pRIOR FILING DATE: 2000-06-30
pRIOR APPLICATION NUMBER: 09/503,387
pRIOR FILING DATE: 2000-02-14
pRIOR FILING DATE: 1990-12-06
pRIOR APPLICATION NUMBER: 09/454,824
pRIOR FILING DATE: 1999-12-06
pRIOR APPLICATION NUMBER: 09/345,468
                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 78
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 61
LENGTH: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: BUSFIAND et al.
PITTE OF INFERTION: GLYCOPROTEIN VI AND USES
FILE REFERENCE: 7853-834
CURRENT APPLICATION NUMBER: US/09/8-3-312
CURRENT FILING DATE: 2001-04-09
                                                                        Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nee 61, Application
No. 6548741
                                   1 SYWMS 5
SMMYS
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Pred. No. 2.5e+05;
Mismatches 0;
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RESULT 2 US-07-942-245-37

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Sequence 37, Application US/07942245
Patent No. 5639641
GENERAL INFORMATION:

APPLICANT: PEDERSEN, Jan T.
APPLICANT: SEARLE, Stephen
APPLICANT: REES, Anthony
APPLICANT: ROGUSKA, Michael
APPLICANT: GUILD, Braydon
TITLE OF INVENTION: SURFACE FINEBRION: ANTIBODIN
NUMBER OF SEQUENCES: 522
CORRESPONDENCE ADDRESS:

Stephen M.J.
Anthony R.
Michael A.
Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES

ADDRESSEE:

Sughrue, Mion, Zinn, Macpeak & Seas

STREET: 2100 Pensylvania Avenue, N.W.

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US-08-545-809A-95
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GENERAL INFORMATION:
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING LITTION: 550
CLASSIFICATION: 550
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 10707-7060
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CONTROL OF THE PROPERTY OF THE
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MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
                                                                                                                             NAME: Freeman, John W.
REGISTON NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUWAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: HP YOUR
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 293-7860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 09-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02110-2804
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                                                                                                 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 SYWMS 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SYMMS 5
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                                                                                                     617-542-8906
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Query Match
Best Local Similarity
Watches 5; Conserve
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US-09-079-029-10
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                                                                                                           RESULT 5
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                                          Sequence 23, Application Patent No. 5874540 GENERAL INFORMATION:
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Patent No. 6342369
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 312 amino acid
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Windatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
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APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: HANSEN, APPLICANT: ARMOUR, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                         70 SYWMS
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Amino Acid
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California
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                                                                                                                                                                                                                                                                                                   Linear
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Hans J.
Kathryn L.
CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
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100.0%; Pred. No. 1.1
tive 0; Mismatches
                                                                                                                                                                                                                                       100.0%; Score 31; DB 4;
100.0%; Pred. No. 2.7e+02;
                                                                              US/08318157E
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                                                                                                                                                                                                                                                     Length 312;
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TITLE OF INVENTION:

MOUSE MONOCLONAL ANTIBODIES: 58

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Best Local Similarity
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Sequence 83, App
- No. 5597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                   atent No. 5597710
GENERAL INFORMATION:
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                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 1:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                   APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
TITLE OF INVENTION: Humanize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                     TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT: Dalie, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: SAXE, Bernhard D. REGISTRATION NUMBER: 28,665 REFERENCE/DOCKET NUMBER: 18
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CLASSIFICATION:
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APPLICATION NUMBER:
                                               APPLICATION NUMBER: FILING DATE: March
                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/318,157B FILING DATE: 05-OCT-1994
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2000 Galloping Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 amino acids
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3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                               Tindall, Stephen
VENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
                                                                                                                                                                                                                                                                                                                                                                Miller, Kenneth
                                               March 10, 1994
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                                                              US/08/208,886C
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Pred. No. 2.5e+05
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                                                                                US-08-208-886C-87
Query Match
Best Local Similarity 80.u
Conservative
                                                                                          TELEFAX: 908 298 5388
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0
FILING DATE: MATCH 10, 1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 908 298 2987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dalie, Barbara
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nicholas
APPLICANT: Tindall, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 908 298 2987
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REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                   TELEPHONE: you 10 10 NO;
                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 07033-0530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Kenilworth
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2000 Galloping Hill Road
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                               90.3%;
                                                                                                                                                                                                                                                                 32,364
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             Score 28; DB 1; Length 10; Pred. No. 39; Indels 1; Mismatches 0; Indels
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Pred. No. 39;
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US-08-704-744-89
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                                                                                                                                           Sequence 89, Application US/08704744 Patent No. 5705154
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Best Local :
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                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                               Matches
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OPERATING SYSTEM: Macintosh 7.5.3
SOPTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,744
FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/02400
FILING DATE: 08-MAR-1995
ATTORNESY/AGENT INFORMATION:
NAME: TC::110- CYNTHIA I.
                                           GENERAL INFORMATION:
APPLICANT: Dalie, Kenneth
APPLICANT: Miller, Kenneth
APPLICANT: Murgolo, Nichola
APPLICANT: Tindall, Stepher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: JB0429K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
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APPLICANT: Tindall, Stephen
                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
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APPLICANT: Miller, Kenneth
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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2000 Galloping Hill Road
Murgolo, Nicholas
Murgolo, Nicholas
Tindall, Stephen
VENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
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Pred. No.
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US-08-469-557-64
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FILING DATE: 06-SEPT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/208886
FILING DATE: 10-MAR-1994
APPLICATION NUMBER: PCT/US/95/0240
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                APPLICANT: Zavodny, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US/95/02400 FILING DATE: 08-MAR-1995 ATTORNEY/AGENT INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: JB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 298-2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schering-Plough Corporation
STREET: 2000 Galloping Hill Road
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MEDIUM TYPE: Floppy disk
                                                                                                                                                NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                  STREET: ZVVV
CTTY: Kenilworth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (908) 298-5388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Kenilworth
                                                                 COUNTRY:
                                                                                                                                  ADDRESSEE:
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                                                                                                                             : M11...
:: Murgolo, N1...
/T: Nguyen, Hanh
/T: Tindall, Stephen
ANT: Tavodny, Paul
ANT: Zavodny, Paul
ANT: MUZENTION: Cloring and Expression of
Yalinst Humanized Monoclonal Antibodies
Yalinst Human Interleukin-4
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                                                                              New Jersey
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                                                                                                                 E: Schering-Plough Corporation
2000 Galloping Hill Road
                                                                  USA
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Miller, Kenneth
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    Mismatches

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Best Local S
Matches 4
                                                                                                                                                                                                                            Sequence 68, Appliant No. 5770403
                                                                                                                                                                                              Patent No. 5770403
GENERAL INFORMATION:
APPLICANT: Dalie,
                    APPLICANT: Murgolo, Manh
APPLICANT: Nguyen, Hanh
APPLICANT: Tindall, Stephen
APPLICANT: Zavodny, Paul
TITLE OF INVENTION: Cloning and Expression of
TITLE OF INVENTION: Humanized Monoclonal Antibodies
TITLE OF INVENTION: Against Human Interleukin-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
TELEPAX: 908-298-5388
                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Foulke, Cynthia L. REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
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APPLICATION NUMBER: U
FILING DATE: 03-JUL-1
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               ADDRESSEE:
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4; Conserv
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Miller, Kenneth
Murgolo, Nicholas
Nguyen, Hanh
3: Schering-Plough Corporation
2000 Galloping Hill Road
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19-FEB-1992
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FIMBER: PCT/US93/01301
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21-MAY-1990
MBER: PCT/US88/03631
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24-OCT-1991
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3-1991
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3ER: 24
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RESULT 12
US-08-290-793B-64
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                                                                                                                                                                                                                    Sequence 64, Application US/08290793B Patent No. 5863537
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Dalie, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 06/
FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
NAME: FOULKe, Cynthia L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/290,793
FILING DATE: August 16, 1994
APPLICATION NUMBER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                             APPLICANT:
                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                               APPLICANT:
                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-JUL CLASSIFICATION: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Foulke, Cynthia L. REGISTRATION NUMBER: 32,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 14-FEB-1991
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FILING DATE: 21-OCT-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07 FILING DATE: 21-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 24-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
NT: Le, Hung
NT: Miller, Kenneth
NT: Murgolo, Nicholas
ANT: Nguyen, Hanh
ANT: Tindall, Stephen
ANT: Zavodny, Paul
OF INVENTION: Cloning and Expression of
TNVENTION: Humanized Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                             1 SYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
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August 16, 1994
JMBER: PCT/US93/01301
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28; DE
Pred. No. 39;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                         Matches
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FILING DATE: AUGUST 16, 1994
PRIOR APPLICATION UNMER: PCT/US93/01301
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/841,659
FILING DATE: 19-FEB-1992
APPLICATION NUMBER: US 07/782,784
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/499,327
FILING DATE: 21-OCT-1991
APPLICATION NUMBER: PCT/US88/03631
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/655,966
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/613,623
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/613,623
FILING DATE: 14-FEB-1991
APPLICATION NUMBER: US 07/615,966
FILING DATE: 16-OCT-1987
APPLICATION NUMBER: US 07/613,623
FILING DATE: 26-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 26-OCT-1987
APPLICATION NUMBER: US 06/881,553
PILING DATE: 03-UUL-1986
APPLICATION NUMBER: US 06/843,958
PILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
APPLICATION NUMBER: US 06/799,668
PILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.
SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
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CITY: Kenilworth
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                                                                   APPLICANT:
                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Foulke, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 2409K7
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2000 Galloping Hill Road
Murgolo, Nicholas
Nguyen, Hanh
Tindall, Stephen
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                   Le, Hung
Miller, Kenneth
                                                                                                         Dalie, Barbara
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US-08-767-128-2

Sequence 2, Application US/08767128 Patent No. 6111079

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GENERAL INFORMATION:

APPLICANT:

WYLIE, DWANE E. LOPEZ, OSVALDO MURRAY, PETER JOSEPH

APPLICANT:

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                                                                                                                                   US-08-290-793B-68
                                                                Matches
                                                                              Query Match
Best Local Similarity
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FILING DATE: 03-JUL-1986
APPLICATION NUMBER: US 06/843,958
FILING DATE: 25-MAR-1986
APPLICATION NUMBER: US 06/799,668
FILING DATE: 19-NOV-1985
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     TELEFAX: 908-298-5388
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                    NAME: FOULKe, Cynthia L.
REGISTRATION NUMBER: 32,364
REFERENCE/DOCKET NUMBER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908 298-2987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 07033-0530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/290,793B
FILING DATE: AUGUST 16,1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Microsoft Word 5.1A
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/I
FILING DATE: 21-OCT-1988
APPLICATION NUMBER: US 0
FILING DATE: 14-FEB-1991
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OPERATING SYSTEM: Macinto
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                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                    ENGTH:
                                                                4
                                                                                                                                                                                amino acid
                                 SYWMS 5
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2000 Galloping Hill Road
                                                                                                                                                                                                    10 amino acids
                                                                Conservative
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                                                                                  90.3%;
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Humanized Monoclonal Antibodies
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                                                                                Score 28; DB 2; Length 10; Pred. No. 39;
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Query Match
Best Local Similarity
Thes 4; Conserve
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US-08-767-128-8
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                                                                                        Sequence 8, Applic
Patent No. 6111079
                                         GENERAL INFORMATION:
APPLICANT: WYLIE,
APPLICANT: LOPEZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US96/09258
                                                                                                                                                                                                                                                                                                                                                     MOLECULE NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
APPLICATION NUMBER: 08/462,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767
                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: sin
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Carter, Charles REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 05-JUN-1996
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                                                                                                                                                                                   31 SYWMN
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                                                                                                        Application US/08767128
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                                                                                                                                                                                                                                                Conservative
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              MURRAY, PETER JOSEPH
GOEBEL, PETER
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                                            , DWANE E.
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LEAD BINDING POLYPEPTIDES AND
NUCLEOTIDES CODING THEREFORE
LEAD BINDING POLYPEPTIDES AND
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                                                                                                                                                                                                                                                             Score 28; DB 3;
Pred. No. 3.5e+02;
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TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRACHENT TYPE: internal

ORIGINAL SOURCE:

US-08-767-128-8
                                                                     밁
                                                                                                 Ś
Search completed: January 12, 2004, 07:03:57 Job time : 6.14062 secs
                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/767,128 FILING DATE: CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/1 FILING DATE: 05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 04-DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                   31 SYWMN 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minneapolis
                                                                                                SMMXS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B: Merchant, Gould, Smith, Edell, Welter & Schmidt
3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                            118 amino acids
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                                                                                                                                     Conservative
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                                                                                                                                                     90.3%;
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                                                                                                                                                     Score 28; I
Pred. No. 3
                                                                                                                                       Mismatches
                                                                                                                                                     DB 3;
3.5e+02;
                                                                                                                                                                       Length 118
                                                                                                                                       Indels
                                                                                                                                     0;
                                                                                                                                     Gaps
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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7: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
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10: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
12: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
13: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
14: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
15: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
16: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
17: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
18: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
20: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
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31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1107863 seqs, 158726573 residues
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1107863
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ø	æ	7	6	ហ	4.	ω	2	1	Result No. So
31	31	31	31	31	31	31	31	31	Score
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		Query Match Length DB
117	98	98	98	98	98	98	ហ	ഗ	ngth
16	23	23	21	21	16	15	24	22	BB
AAR66301	ABG78210	ABG91901	AAB40140	AAB40138	AAR72074	AAR52066	ABU11259	AAB61293	ID
Human immunoglobul	Human Fv molecule	Human antibody fra	Anti-hIL12 antibod	Anti-hIL12 antibod	DP54 VH region. H	Heavy chain variab	Human TANGO 268 VH	Anti-TANGO 268 scF	Description

Mouse germiine nea Human immune/haema	AAE06973 AAM83420	22	103	90.3	288	44
Human tyr	7560	ν ν ν	100	90.3	S 82	43
Human typ	560	23	88	•	28	42
Human typ	AAU75600	23	79	•	28	41
BONT/A Ho	ABU56854	24	66		28	40
BONT/A Ho	ABU56853	24	66	•	28	39
BONT/A Ho	ABU56852	24	66	٠	28	38
BONT/A Ho	ABU56851	24	66	•	28	37
BONT/A Ho	ABU56835	24	66	•	28	36
Human 5'	AAY64781	21	59		28	35
Human pep	ABG40558	23	46	•	28	34
Peptide #	AAM18657	22	46	•	28	ω u
Human ty	AAU75604	23	20		28	32
Anti-NKG2D	AAU72831	23	10	•	28	32
22A5 IgM heavy	35	23	ភ	•	28	30
Human FAPalpha	9	23	5	•	28	29
Tumour antigen		20	5	•	28	28
Humanised	AAR97316	17	տ	•	28	27
Scfv (FWP51)	AAR85499	16	տ	•	28	26
C glutamicum	AAG90944	22	395	•	31	25
Single chain	ABG74385	24	312	•	31	24
Amino acid	ABB09604	23	312	•	31	23
	AAW83323	20	312	•	31	22
cl	810	20	271	•	31	21
ä	515	23	O.	•	31	20
	515	23	265	•	31	19
О	514	23	g	•	31	18
Protein for	AAU75152	23	264		31	17
	ABP45583	23	251	•	31	16
Human BLyS	ABP45459	23	247	•	31	15
Human BL	87	23	4	•	31	14
Human HIV-	AAB62776	22	125	•	31	13
	Ð	22	N	•	31	12
Human HIV	AAB62777	22	123	100.0	31	11
S. aureus	AAE25526	23	μ	•	31	10

## ALIGNMENTS

XX XX	×	PR	PR	PR	×	ΡF	×	Dď	×	PN	X	20	X	X	X.	\$	Š	\$	X	Š	X	DH	×	D	×	AC	×	AAB61293	RESULT 1
(MILL-) MILLENNIUM PHARM INC.		20		30-JUN-1999; 99US-0345468.		30-JUN-2000; 2000WO-US18152.		04-JAN-2001.		WC200100810-A1.		Homo sapiens.		cancer.	ischaemia; cardiovascular disease; immunological disease; liver disorder;	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;	platelet membrane glycoprotein receptor; bleeding disorder;	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;	TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;	Human; antibody; scFv; CDR; complementarity determining region;		Anti-TANGO 268 SCFV CDR, SEQ ID NO: 61.		04-APR-2001 (first entry)		AAB61293;		1293 AAB61293 standard; Peptide; 5 AA.	LT 1

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RESULT 2
ABU11259
ID ABU1
XX ABU1
XX ABU1
XX ABU1
XX Huma
XX Corng
XW Corng
XW 1eg
XW 1eg
XW Cerr
XX Hom
XX 
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thrombombolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; leg swelling; pain; ulceration; pectors; myocardial infarction; cardiovascular disease; angina pectors; myocardial infarction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent acture cardiac ischaemia following angioplasty and metastatic cancers, especially of the colon and liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycoprotein VI, and its me and diagnosing hemorrhagic immunological disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is nucleic acid molecule en glycoprotein VI (GPVI),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, trand diagnosing hemorrhagic disorders, thrombotic diseases and
                                                                                                                 09-APR-2001; 2001US-0829495.
                                                                                                                                                                                             09-APR-2002; 2002WO-US11122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coronary restenosis; atherosclerosis; immunological disorder; developmental disorder; embryonic disorder; liver disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TANGO 268 VHCDR1 Peptide #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 31; Page 102; 227pp;
                                                                                                                                                                                                                                                                              17-OCT-2002
                                                                                                                                                                                                                                                                                                                                                       WO200280968-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cerebral vascular
                                    (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABU11259 standard; Peptide; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SYWMS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ហ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Villelal J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ம
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease; venous thromboembolism disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 9.3e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5;
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Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
                                                                                                                                                                           Busfield SJ, Villeval Qian DM, Kingsbury G;
                                                                                                                                                                                                            Villeval
                                                                                                                                                                                                            Ç
                                                                                                                                                                                                            Jandrot-Perrus M,
                                                                                                                                                                                                            Vainchencker W,
                                                                                                                                                                                                               Gill DS;
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Disclosure; Page 111; 236pp; English

CC Collagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration. CC morphology, differentiation and/or function of megakaryocytes and CC platelets, including during development e.g. embryogenesis, modulating CC leukocyte-platelet and platelet-endothelium interactions in CC inflammation and/or thrombosis, and modulating platelet aggregation and CC with abnormal or aberrant megakaryocyte and/or platelet aggregation and CC with abnormal or aberrant megakaryocyte and/or platelet proliferation, CC migration, morphology, differentiation and/or function, e.g. bleeding CC disorders such as thrombocytopaenia. Other diseases which may be CC modulated by these antibodies are thrombotic disorders, cerebral CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism CC diseases (e.g. diseases involving leg swelling, pain and ulceration, pulmonary embolism, etc); coronary diseases (e.g. cardiovascular CC diseases including angina pectoris, myocardial infarction, coronary CC restenssis, atherosclerosis, etc); immunological disorders, cerebral CC developmental disorders, embryonic disorders, liver disorders, cerebral CC vascular diseases, venous thromboembolism disease, coronary diseases, cardiovascular CC restensies in platelet counts, platelet aggregation, and/or platelet activation and so have some advantages over prior art comethods. The present sequence represents a peptide sequence used to CC generate the antibodies of the invention. variable heavy (VH) complementarity determining region (CDR)1, VH CD or VH CDR3, or variable light (VL) CDR1, VL CDR2 or VL CDR3, and immunospecifically binding to a TANGO 268 (also referred as glycopro VI (GPVI)) antigen. The antibodies of the invention act to decrease block TANGO 268 binding to extracellular matrix components, or as a collection of the components of t This invention relates to a novel purified antibody comprising a variable heavy (VH) complementarity determining region (CDR)1, VI or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and generate the antibodies of the invention. as glycoprotein CDR2 ö

Sequence v A,

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Query Match
Best Local S
Matches 5
          Similarity
 <u>ن</u>
 Conservative
100.0%; Score 31;
100.0%; Pred. No.
tive 0; Mismatch
   Mismatches
 9.3e+05;
                    DB 24;
                   Length
   Indels
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SMMAS
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1 SYWMS

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RESULT 3
AAR52066
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AAR52066 standard; Protein; 86

AAR52066;

11-OCT-1996 (first entry)

Heavy chain variable region of human PL0123 antibody.

antibody; humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping; modelling; surface residue; modify. Region Homo sapiens Location/Qualifiers /label= framework_region_l /note= "FR 1"

4%

Region

/note= 50..59

36..49 note=

/note=

"CDR 2" "FR 2" "CDR Region

31..35 /label=

complementarity_determining_region_1

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Best Local (
                                              Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
                                                                                                                                                                                                                                                                                                                                                                  order to produce a humanised rodent Ab can be determined by calculating homology between murine and human Ab antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up: (1) traditional loop grafting; (2) resurfacing approach using most similar chain; and (3) resurfacing approach using human sequences with most similar surface residues. The Ab used was the murine anti-N901 Ab (see AARS2061). Experiment 3 was carried out using the present sequence which represents the human PLO123 Ab light chain variable region with 74 percent homology with anti-N901 Ab. N901/PL0123 (AARS2067) was prepd. by resurfacing. Sequence numbering starts at possition 118 in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Guild BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1993;
                         Homo sapiens
                                                                                                DP54 VH region
                                                                                                                        25-MAR-2003
26-SEP-1995
                                                                                                                                                              AAR72074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 4B; 230pp; English.
                                                                                                                                                                                    AAR72074 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modification of a rodent antibody (Ab)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP592106-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1994-120230/15
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                                                                                                                                                                                                                                                                                             Similarity
5; Conserv
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                                                                                                                                                                                                                                                 SMMYS
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                                                                                                                                                                                                                                                                                                                                               98 AA;
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                                                                                                                        (updated)
(first en
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  Location/Qualifiers
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                                                                                                                                                                                    Protein;
                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                          Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ab can be determined by calculating
                                                                                                                                                                                                                                                                                                         1.4e+02;
                                                                                                                                                                                                                                                                                                                       DB 15;
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                                                                                                                                                                                                                                                                                                                     Length 98;
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RESULT 5
AAB40138
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                          Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory; complementarity determining region; CDR; antirheumatic; antiarthritic; antiasthartic; neuroprotective; antipsoriatic; antiasthartic; cardiant; antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF7H1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  showed homology to the germline gene DP54 (AAQ89332), which encodes the protein given in AAR72074. The DNA (AAQ89333) and corresp. amino acid (AAR72075) sequences of the VH region of a representative clone,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 2/15 clones of H chain (IGG1) genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graves' ophthalmopathy-associated monoclonal by molecular cloning of immunoglobulin genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 72; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                       24-MAR-2000; 2000WO-US07946.
                                                                                                                         Homo sapiens.
                                                                                                                                               multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                    Anti-hIL12
                                                                                                                                                                                                                                          05-FEB-2001
                                                                                                                                                                                                                                                                AAB40138;
                                                                                                                                                                                                                                                                                      AAB40138 standard; Protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-139383/18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAR-1995
                                  25-MAR-1999;
                                                                                                  WO200056772-A1
(BADI ) BASF AG.
(GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (NICH-) NICHOLS INST DIAGNOSTICS.
                                                                                                                                                                                                                                                                                                                                               31 SYWMS
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                                                                                                                                                                                                                                                                                                                                                                    SWMYS 1
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                                                                                                                                                                                                                   ant ibody
                                                                                                                                                                                                                                                                                                                                                                                                                                        98 AA;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                         (first entry)
                                  99US-0126603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41..44
/label= CDR1
49..67
/label= CDR2
                                                                                                                                                                                                                   H chain V region amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                           0;
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: Pred. No. 1.4
0; Mismatches
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genes by PCR
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                                                                                                                                                                                                                    SEQ ID
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                                                                                                                                                                                                                    664.
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cc interleukin-12 (IL-12). The invention also includes antigen binding CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human CC anti-IL-12 antibody heavy and light chain complementarity determining region (CDR) amino acid sequences, and also includes variable region CC given in AAB39517-B39560 and AAB40068-B40149. Sequences are CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39772-B40063 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 crepresent other CDR sequences. Light chain CDR3 consensus sequences are CC given in AAB40064-B40067. Primers used in the identification and CC construction of the antibodies of the invention are given in CC AAC61062-C61071. The antibody of the invention are given in CC antibody and has antirheumatic; antiarthritic; antisclerotic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. CC antihodises or antigen-binding fragments are useful in the treatment CC of disorders associated with detrimental release of human IL-12. CC They can also be used in the manufacture of a pharmaceutical composition CC to treat human IL-12 disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
AAB40140
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Best Local S
Matches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Salfeld JG, Roguska M, I
Kaymakcalan Z, Labkovsky
Veldman GM, Venturini A,
                                                                                                                                                                                                                                                   complementarity determining region; CDR; antirheumatic; antiarthritic; antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant antiparastic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 75; Page 122; 377pp; English.
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                                               24-MAR-2000; 2000WO-US07946
25-MAR-1999;
                                                                                                                                                     WO200056772-A1
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                         Human; neutralising antibody; interleukin-12;
                                                                                                                                                                                                                                                                                                                                                                                                      Anti-hIL12 antibody H chain V region amino acid sequence SEQ ID
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ilarity 100.0%;
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99US-0126603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
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cy B, Sakora
A, Warne NW,
S, Smith S,
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    Sakorafas P, Friedrich S, M
    Sakorafas P, Friedrich S, M
    srne NW, Widom A, Elvin JG, M
    nith S, Holtet TL, Du Fou SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 21;
Pred. No. 1.4e+02;
; Mismatches 0;
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CC This invention relates to a new human antibody specific for human CC interleukin-12 (IL-12). The invention also includes antigen binding CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human CC anti-IL-12 antibody heavy and light chain complementarity determining CC region (CDR) amino acid sequences. Other variable region includes variable region CC amino acid sequences. Other variable region amino acid sequences are CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39771 CC represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and CC construction of the antibodies of the invention are given in AAB40064-B40067. Primers used in the identification and CC AAC61062-C61071. The antibodies of the invention is a neutralising CC antibody and has antirheumatic; antispartatic; antiacthratic; antischerotic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. CC The antibodies or antigen-binding fragments are useful in the treatment of disorders associated with detrimental release of human IL-12, CC They can also be used in the manufacture of a pharmaceutical composition to treat human IL-12 disorders.
                                                         Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human antibody specific for human interleukin-12 treat disorders characterized by aberrant IL-12 expre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Veldman GM,
Derbyshire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salfeld
                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 75; Page 122; 377pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n Z, Hamini A
, Venturini A
s EJ, Carmen (
                                                           98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roguska M, Paskind M, Banerjee S, Tracey DE, Whit, Z, Labkovsky B, Sakorafas P, Friedrich S, Myles A; Venturini A, Warne NW, Widom A, Elvin JG, Duncan J, Carmen S, Smith S, Holtet TL, Du Fou SL;
                                                           A,
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sclerosis
Score 31;
Pred. No.
                      BB
                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression
                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IL-12) used to ession e.g. Crohn's
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Matches
31
             1 SYWMS 5
                          Similarity
5; Conserv
SMMS
                           Conservative
35
                           0
                           . 1.4e+02;
thes 0;
                            Indels
                            0,
                            Gaps
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0

밁 S

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Human antibody fragment #85
                                                       04-DEC-2002
                                                                  ABG91901 standard; Protein;
                                                       (first entry)
                                                                   98
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Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function sulphated tyrosine-dependent protein-protein interaction. function;

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Homo
sapiens.
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31-DEC-2001; 2001WO-US49442

29-DEC-2000; 29-DEC-2000; 2000US-258948P 2000US-0751181

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(BADI ) BASF

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cc important in physiological phenomena such as cell rolling, metastasis and clinflammation, where the epitope is capable of being bound by an antibody, cc its antigen-binding fragment or its complex comprising at least one can thoody or its binding fragment having a first hypervariable region. The clinguishes are useful for inhibiting cell rolling, inflammation, autoimmune cdisease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell-matrix, platelet-matrix, platelet-matrix, for increasing mortality of tumour or leukaemia cells, for increasing the concerce conceasing mortality of tumour or leukaemia cells, for increasing the cor anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or for decreasing the number of diseases, anti-cancer cor the above mentioned purposes. The epitopes are useful for diseases, conformations of inflammatory diseases such as cancer, leukaemia, autoimmune diseases, conformations and diseases such as myocardial cor inflammatory control diseases caused by sulphated tyrosine-dependent cor protein-protein interactions. This sequence represents a human antibody control of the inventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 5
                                                            31-DEC-2001; 2001WO-US49440
                                                                                                                                   WO200259264-A2
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                               Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adeno lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaem
                                                                                                                                                                                                                                                             Human Fv molecule hypervariable region related peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                29-DEC-2000; 2000US-0751181
                                                                                                                                                                                                                                                                                                   15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                 ABG78210 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 268; 310pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      physiological phenomena suc
inflammation, for treating
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Szanthon E, I
 (BIOT-) BIO-TECHNOLOGY GEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BIOT-) BIO-TECHNOLOGY GEN
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les 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYWMS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relates to an
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lichter T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epitope present on cance
phenomena such as cell refor treating autoimmune,
                                                                                                                                                                                                                                                                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plaksin D, Vogel T, Amit B, Kooperman L,
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                                                                                                                                                                                                                                                                                                                                                                   98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 31; DB 23;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on cancer cells and important in s cell rolling, metastasis and oimmune, inflammatory or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epitope present on cancer contains, metas such as cell rolling, metas
                                                                                                                                                                                                 sarcoma; leukaemia; adenoma;
oma; acute myeloid leukaemia.
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Peretz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 98;
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                                                                                                                                                                                                                                                                #85
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Levanon A;
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RESULT 9
AAR6301
ID AAR6
XX AAR6
AC AAR6
AC AAR6
DT 25-M
DT 02-A
XX Prim
KW Cosm
KW Cosm
KW Cosm
KW WO94
XX Homc
XX Ho
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Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell). The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region
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Plaksin D,
DNA fragment comprising human immunoglobulin Vh production of human immunoglobulin in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                  N-PSDB; AAQ78946.
                                                                                                             WPI; 1995-006791/01.
                                                                                                                                                                                                                                                                                                                                                                                                   24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9426895-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cosmid; placenta; vector; pJB81; E.coli; mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunoglobulin variable heavy chain #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
02-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR66301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells
                                                                                                                                                                                                                                                                                   10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                           10-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        related peptide of the invention.
                                                                                                                                                                                                                           (NISB)
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les 5; Conserv
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                                                                                                                                                                                                                              JAPAN TOBACCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYWMS 35
                                                                                                                                                                     Matsuda F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lazarovits
. Peretz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA,
                                                                                                                                                                                                                                                                                      93WO-JP00603
                                                                                                                                                                                                                                                                                                                                              93WO-JP00603.
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipschitz O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Szanton E,
  genes
hosts
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                             for
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Claim 17; Page 40-41; 130pp; Japanese.

sequences (AAR66295-51)

are

novel

human immunoglobulin heavy

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RESULT 10
AAE25526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC chain sequences encoded by novel isolated genes. The genes CC (AAQ78939-79002) were isolated and cloned from a series of cosmid CC constructs: Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M131, by PCR CC amplification using primers AAQ78917-38. The genes are subdivided into 5 (amplification using primers AAQ78917-38. The genes are subdivided into 5 (amplification using primers AAQ78917-38. The genes are subdivided into 5 (c) families of Vn genes. The fragments cover a region of 800 kb. The DNA CC fragments were isolated from high molecular weight DNA from human cc placenta. The DNA was partially digested with TaqI restriction enzyme. CC were collected. The fragments were ligated with ClaI-digested cosmid CC were collected. The fragments were ligated with ClaI-digested cosmid CC vector pJB81. The ligation products were in vitro packed and infected CC into E.coli 490A. The fragments were then subcloned by colony CC useful in producing human immunoglobulin in mammalian hosts.

CC (Updated on 25-MAR-2003 to correct PN field.)
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S. aureus Map10 antibody H07VHD-1 (variable heavy chain) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE25526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE25526 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                      Map10 protein; infection; immunological response; passive immunisation; vaccine; antibacterial; variable heavy chain; H07VHD-1 protein.
                        Antibody capable of binding subdomains of Map10 protein, a surface localized protein from Staphylococcus aureus, useful for preventing
                                                                                                                                                                  20-OCT-2000;
21-MAR-2001;
                                                                                                                                                                                                           22-OCT-2001; 2001WO-US32550
                                                                                                                                                                                                                                        02-MAY-2002
                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
           treating
                                                                                                             Patti JM,
                                                                                                                                         (INHI-) INHIBITEX INC.
                                                                                                                                                                                                                                                                    WO200234788-A1
                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                   2002-547435/58.
)B; AAD41846.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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           staphylococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                            Domanski P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                  2000US-241832P.
2001US-277287P.
                                                                                                                                                                                                                                                                                                                                                                                                              aureus
                                                                                                                                                                                                                                                                                                             99..
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         note=
                                                                                                                                                                                                                                                                                                                                                    note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 117
                                                                                                                                                                                                                                                                                                             .106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                          "Complementarity determining
                                                                                                                                                                                                                                                                                                                                                      "Complementarity determining
                                                                                                                                                                                                                                                                                              "Complementarity determining region (CDR)"
              infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 31; DB 16;
Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
              ä
              humans
              õ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                            region
                                                                                                                                                                                                                                                                                                                                                       region
                   for preventing
                                                                                                                                                                                                                                                                                                                                                       (CDR) "
                                                                                                                                                                                                                                                                                                                             (CDR) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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The present sequence relates to novel antibodies which are capable of CC binding to the subdomains Map10 protein, a surface localised protein CC prom Staphylococcus aureus. Sequences of the invention prevent S. aureus infection in a human or animal and inhibit binding of staphylococcal bacteria to eukaryotic cells. They are also useful for diagnosing an CC infection of S. aureus in a sample and for treating or preventing S. aureus in a sample and for treating or preventing S. aureus in fection in humans or animals. Antibodies of the invention are useful CC identifying antibodies to the Map10 protein in a sample. They are also CC useful in preventing adherence of Staphylococcal bacteria, in production CC facilities or laboratories to isolate additional quantities of the CC proteins, such as by affinity chromatography and in the development of CC vaccines for passive immunisation against staphylococcal infections. The contents for passive immunisation against staphylococcal infections. The contents of the make them safer to use, including sutures, replacement heart colves to make them safer to use, including sutures, replacement heart valves, cardiac assist devices, hard and soft contact lenses, intraocular regions implants, other implants such as corneal inlays, kerato-prostheses, cardiac stents, dental prostheses, pacemakers and heart valves. The present sequence is a DNA encoding Staphylococcus aureus Map10 antibody in the protein in the sequence is a DNA encoding Staphylococcus aureus Map10 antibody in the protein in the sequence is a DNA encoding Staphylococcus aureus Map10 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; Page 48; 52pp; English
H07VHD-1 (variable heavy chain) protein.
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Matches
                                 Query Match
Best Local
31 SYWMS 35
             1 SYWMS
                           l Similarity
5; Conserva
                            Conservative
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                                   100
                                  .0%; Score 31;
                            0,
                             Mismatches
                                    DB 23;
1.7e+02;
                             0
                                          Length 117;
                             0,
                              Gaps
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0

Sequence

117 AA;

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RESULT 11
AAB62777
                                                                      03-APR-2001
                                                                                                             AAB62777;
                                                                                                                                                   AAB62777 standard; Protein;
Human immunodeficiency virus-1; HIV-1; human monoclonal antibody.
                                     Human HIV-1 monoclonal antibody
                                                                        (first entry)
                                                                                                                                                      123
                                       SEQ ID NO:
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Homo sapiens envelope glycoprotein; gp120; diagnosis.

04-JAN-2001.

WO200100678-A1

23-JUN-2000; 2000WO-US17327

(USSH ) US DEPT HEALTH & HUMAN SERVICES 30-JUN-1999; 99US-0141701

Watkins BA, Reitz MS;

WPI; 2001-112438/12. N-PSDB; AAF29078.

Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting in biological sample and providing passive immunotherapy to HIV-1 infected mammal HIV-1

Claim 1; Page 70; 81pp; English.

The present invention provides the protein and variable regions of human monoclonal antibodies coding s which sequences for the are immunoreactive

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RESULT 13
AAB62776
ID AAB62
XX
AC AAB62
XX
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AAB62778
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Best Local
                                                                                                                                                           Claim
       AAB62776
                                                                                                           Sequence
                                                                                                                                 with human
                                                                                                                                                                              Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for dein biological sample and providing passive immunotherapy tenders.
                                                                                                                                                                                                                                                                                      04-JAN-2001.
                                                                                                                                                                                                                                                                                                    WO200100678-A1
                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                              envelope glycoprotein;
                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus-1; HIV-1; human
                                                                                                                                                                                                                                                                                                                                                  Human HIV-1 monoclonal antibody SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                              AAB62778;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection.
                    AAB62776
                                                                                                                                              The present invention
                                                                                                                                                                                                                                Watkins
                                                                                                                                                                                                                                                          30-JUN-1999;
                                                                                                                                                                                                                                                                        23-JUN-2000; 2000WO-US17327.
                                                                                                                                                                                                           2001-112438/12.
DB; AAF29079.
                                                                                                                         can be used in
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5; Conserv
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                                                                                Similarity 5; Conserv
                                                                                                                                                                                                                                             S
                                                                                                                       ant invention provides the protein and coding sequences for the regions of human monoclonal antibodies which are immunoreactive an immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. n be used in diagnosis and therapy of HIV-1 infection.
                    standard;
                                                       SMMAS
                                                                   SYMMS 5
                                                                                                                                                           Page
                                                                                                                                                                          mammal
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                                                                                                             123
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                                                                                Conservative
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                                                                                                                                                                                                                               Reitz MS
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                                                                                                                                                          71; 81pp;
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                    Protein;
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                                                                                Score 31; DB Pred. No. 1.8); Mismatches
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Pred. No.
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                                                                                       1.8e+02;
                                                                                              DB 22;
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                                                                                                                                                                                                                                                                                                                                     monoclonal antibody;
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                                                                                             Length 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                               detecting HIV-1
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RESULT 14
ABP45878
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Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting in biological sample and providing passive immunotherapy to HIV-1
                                                                                                                                                                                             systemic lupus erythematosus; rheumatoid arthritis; CVID; common variable immunodeficiency; acquired immunodeficienc
                                                                                                                                                                                                                                                                                                                                                                Human BLyS binding scrv SEQ ID 1889
                                                                                                                                                                                                                                                                                                                                                                                                                  19-AUG-2002
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                                                      10-JAN-2002.
                                                                                                   WO200202641-A1
                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP45878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP45878 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUN-1999;
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15-JUN-2001; 2001WO-US19110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein; 241
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Pred. No. 1.8e+02;
; Mismatches 0;
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                                                                                                                                                                                                immunodeficiency syndrome.
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16-JUN-2000; 2000US-212210P

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RESULT 15
ABP45459
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16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                         BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatio; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                         19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                       ABP45459 standard; Protein; 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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16-JUN-2000;
17-OCT-2000;
                                              15-JUN-2001;
                                                                                                                                                                                                                                                                                         Human BLyS binding
                                                                                                              WO200202641-A1
                                                                                                                                            Homo sapiens.
                                                                                                                                                                             common variable
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                                                                              10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SYWMS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 AA;
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2001US-276248P.
2001US-277379P.
2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
2000US-212210P.
2000US-240816P.
                                                2001WO-US19110
                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35
                                                                                                                                                                          immunodeficiency; acquired immunodeficiency syndrome
                                                                                                                                                                                                                                                                                           BCFV SEQ ID 1470.
                                                                                                                                                                                                                                                                                                                         entry)
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Pred. No. 3.4e+02;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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Search completed: January 12, Job time: 14.1094 secs

2004, 06:58:52

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Best Local S
Matches 5
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                                                                                                                                                                                 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (cVID) and immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 2157-2158; 3148pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben
                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                               Local Similarity
nes 5; Conserv
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31
                               1 SYWMS 5
SMMYS
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                                                                                                                                   247
                                                                Conservative
                                                                                                                                 A,
                                                                Choi GH,
                                                                                  Score
Pred.
                                                                  Mismatches
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No.
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Title:
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Maximum DB seq length: 200000000
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Maximum Match 10
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1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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10: /cgn2=6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2=6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

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18: /cgn2=6/ptodata/1/pubpaa/US09_PUB.pep:*

18: /cgn2=6/ptodata/1/pubpaa/US09_PUB.pep:*
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1 SYWMS 5
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9 US-09-832-312-61

12 US-10-308-817-55

2 US-10-308-817-55

2 US-10-029-9888-85

2 US-10-032-0378-85

2 US-10-032-0378-85

2 US-10-194-975-15

5 US-10-194-975-15

6 US-09-982-992A-6

1 US-09-982-992A-6

1 US-09-980-748-189

1 US-09-880-748-189

1 US-10-322-673-48

US-10-288-917-10

US-10-288-917-10
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                                                                                                                                                  Sequence 61, Appl
Sequence 61, Appl
Sequence 55, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 85, Appl
Sequence 15, Appl
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Sequence 6, Appli
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    Sequence
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Sequence
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15, Appl
6, Appli
1889, Ap
1470, Ap
1470, Ap
148, Appl
1594, Ap
10, Appl
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## ALIGNMENTS

US-09-832-312-61

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; SEQ ID NO 61
; LENGTH: 5
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-832-312-61
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234
CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
FRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30
PRIOR PRIOR APPLICATION NUMBER: 09/503,387
PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR FILING DATE: 1909-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
RESULT 2
US-09-829-495-61
; Sequence 61, Application US/09829495
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                        1 SYWMS 5
1 SYWMS 5
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100.0%; Pred. No. 6.0
vative 0; Mismatches
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TITLE OF INVENTION: WISSELL
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: Patentin version 3.1
SEQ ID NO 55
LENGTH: 98
TYPE: DOT
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                                                                                                         US-10-029-988B-85
                                                                                                                             RESULT 4
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US-10-308-817-55
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CURRENT APPLICATION NUMBER: US/09/829,495

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 09/610,118

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/503,387

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR FILING DATE: 1999-12-06

PRIOR FILING DATE: 1999-12-06
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Sequence 85, Application US/10029988B
Publication No. US20040001839A1
GENERAL INFORMATION:
APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 55, Application US/10308817
Publication No. US20030219861A1
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
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Pred. No. 3e+02;
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Pred. No. 6.6e+05;
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Best Local S
Matches 5
              APPLICANT: Bio-Technology General Corp.
TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
FILE REFERENCE: 10793/45
CURRENT APPLICATION NUMBER: US/10/032,423A
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 12/29/2000
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 98
TYPE: PRT
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Publication No. US20040001822A1

GENERAL INFORMATION:

APPLICANT: Bio-Technology General Corp.

TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED

TITLE OF INVENTION: MOLETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF

FILE REFERENCE: 10793/44

CURRENT APPLICATION NUMBER: US/10/032,037B

CURRENT FILING DATE: 2001-12-31

PRIOR APPLICATION NUMBER: 60/258,948

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 204
SOPTWARE: FRSTSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 98
TYPE: PRT
                                                                                                                                                                                                                                                                                Sequence 85, Application No. US200 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 98
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CURRENT APPLICATION NUMBER: US/10/029,988B
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/258,948
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 204
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                      Application US/10032423A
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RESULT 9
US-09-995-529-8
; Sequence 8, Application US/09995529
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Best Local S
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LENGTH: 98
TYPE: PRT
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Best Local Similarity
Matches 5; Conser
                                                                                                                                                                                     Matches
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SEQ ID NO 6
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/10194975
Publication No. US20030039649A1
GENERAL INFORMATION:
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TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO THE MAP PROTEIN AND METHOD OF USE IN TRE
TITLE OF INVENTION: AND PREVENTING INFECTIONS
FILE REFERENCE: PO6922US02/BAS
CURRENT APPLICATION NUMBER: US/09/982,992A
CURRENT FILING DATE: 2001-10-22
CURRENT FILING DATE: 2001-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Super Humanized Antibodies FILE REFERENCE: 501231.01 CURRENT APPLICATION NUMBER: US/10/194,975 CURRENT FILING DATE: 2002-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/277,287
PRIOR FILING DATE: 2001-03-21
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SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/305,111 PRIOR FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/241,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Foote, Jefferson
                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Staphylococcus aureus
                                                                                                         31
                                                                                                                                              1 SYWMS 5
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5; Conserv
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                                                                                                                                                                                                                        Length 117;
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                                                                                                                                          RESULT 11
US-09-880-748-1470
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US-09-880-748-1889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
                                                                              Sequence 1470, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 1889
LENGTH: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 120
TYPE: PRT
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Best Local
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/995,529
CURRENT FILING DATE: 2001-11-26
NUMBER OF SEQ ID NOS: 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/293,499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Humanized Collagen Antibodies and TITLE OF INVENTION: Related Methods FILE REFERENCE: P-IX 4976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Huse, William APPLICANT: Tang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   y Match 100.0%; Score 31; DB 11; Local Similarity 100.0%; Pred. No. 3.5e+02;
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100.0%; Pred. No. 6.:
ative 0; Mismatches
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RESULT 13
US-09-880-748-1594
; Sequence 1594, Application US/09880748
; Publication No. US20030059937A1
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US-10-322-673-48
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; OTHER INFORMATION: CM013F04 SCFV
US-10-322-673-48
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US-09-880-748-1470
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PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                                                                                                                                                           Query Match
Best Local
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PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 48
LENGTH: 247
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SEQ ID NO 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/369,877
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR APPLICATION NUMBER: 60/384,828
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CURRENT FILING DATE: 2002-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL TITLE OF INVENTION: Receptors FILE REFERENCE: PF585
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PRIOR APPLICATION NUMBER: 60/396,591
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/403,370
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PRIOR FILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2002-08-15
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5; Conserv
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Pred. No. 6.3e+02;
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Pred. No. 6.3e+02;
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RESULT 14
US-10-288-917-10
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/10288917
Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT Adams, Camilia W.
Ashkenazi, Avi J.
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PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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                                                         APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity tes 5; Conserv
                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NO. US20030148455A1-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOPTWARE: WildPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1 DNA Way
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                       NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
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Pred. No.
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INFORMATION FOR SEQ ID NO: 10:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-5416 TELEFAX: 650/952-9881

SEQUENCE CHARACTERISTICS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-052-798-10
                                                                             Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/079,029
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHAUG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/25-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 10, Application US/100 Publication No. US20020150985A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 31; DB 12; Best Local Similarity 100.0%; Pred. No. 7.6e+02; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chuntharapai, Anan
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Adams, Camilia W. Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 SYWMS 74
70 SYWMS 74
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                                       1 SYWMS 5
                                                                             Similarity 5; Conser
                                                                                                                                                                                                LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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TYPE: Amino Acid
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
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                                                                           100.0%; Score 31; DB 14; Length 312; ilarity 100.0%; Pred. No. 7.6e+02; Conservative 0; Mismatches 0; Indels
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Search completed: January 12, 2004, 07:19:52 Job time : 15 secs

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Post-processing: Minimum Match 0%
Maximum Match 10
Listing first 45
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Maximum DB
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                                                             Database
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seq length: 2000000000
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PIR 76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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89
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106.117 Million cell updates/sec
                                                                                                                                                                                                                                    283308 seqs, 96168682 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

ry  ch Length DB ID  Description  1. 147 2 137780  1. 197 2 PH0872  1. 198 2 PL01873  1. 110 2 PH1655  1. 117 2 S34886  1. 117 2 S34886  1. 117 2 S31587  1. 118 2 S31587  1. 119 2 S31587  1. 139 2 137781  1. 139 2 137781  1. 139 2 137781  1. 139 2 137781  1. 139 2 137599  1. 130 2 S31599  1. 130 2 S31599  1. 131 2 S31598  1. 132 2 S31598  1. 133 2 S31598  1. 134 2 S31598  1. 135 2 S31588  1. 136 2 S36259  1. 137 2 S36259  1. 138 2 S36259  1. 139 2 S31588  1. 130 2 S31588  1. 131 2 PH1661  1. 131 2 PH1644  1. 132 PH1644  1. 133 PH1644  1. 134 PH1644  1. 1
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DB ID Descript:  2 137780
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71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9	71.9
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S31674	S31679	S31603	PL0098	S38493	831119	E36005	G36005	S19666	S31112	F36005	S31116	S31677	836270	S46392	S46390
Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	j heavy	heavy	ш	j heavy	, heavy	heavy			heavy	_	heavy	heavy	Ig heavy chain V r

## ALIGNMENTS

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-97 < MAN>
C; Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that bear C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 14-97 Domain: immunoglobulin homology < IMN>
F; 30-35 Region: complementarity-determining 1
F; 49-66 Region: complementarity-determining 2
                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: PH0872
R;Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghossein, C.; Smith, A.; Diamond, B. J. Exp. Med. 174, 1639-1652, 1991
J. Exp. Med. 174, 1639-1652, 1991
A;Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiotyp A;Reference number: PH0862; MUID:92078875; PMID:1660528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PH0872
Ig heavy chain V region (anti-DNA, III-3R) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 16-Aug-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNĀ
A;Residues: 1-147 <RES
A;Cross-references: EMBL:X67943; NID:g33578; PIDN:CAA48130.1; PID:g33579
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;28-111/Domain: immunoglobulin homology <IMM>
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C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37780; S25474
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                                Best
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92.1%; Score 82; DB 2; Le
88.2%; Pred. No. 1.5e-06;
Mismatches 1;
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A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL A;Note: the sequence shows the V region (TD-Vr) from a nonproductive DNA rearrangement R;Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G. J. Mol. 227, 776-798, 1992

A;Title: The repertoire of human germline V(H) sequences reveals about fifty groups of A;Reference number: $26885; MUID:93021117; PMID:1404388

A;Accession: $26897
RESULT
S36280
                                                                                                                                                                                                                                                                                                                                                                            R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, B.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulir A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z12354; NID:g32930; PIDN:CAA78224.1; PID:g32931 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM> F;31-35/Region: complementarity-determining 1 F;49-65/Region: complementarity-determining 2
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A; Residues: 1-98 < TOM>
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A; Residues: 1-98 <BIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #tex
C;Accession: PL0123; S26897
R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
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88.2%;
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Pred. No. 1.7e-06;
1; Mismatches 1;
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Pred. No. 1.5e-06;
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               C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_chan
C;Accession: $60299; $17079
R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A.
Immunol. Lett. 34, 57-62, 1992
A;Title: Immunoglobulin heavy and light chain gene sequences
A;Reference number: $60295; MUID:93122853; PMID:1282498
A;Accession: $60299
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S17079
Ig heavy chain V-gene (clone HHG19) -
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C;Date: 03-Feb-1998 movement of the control of the 
                                                                                                                                                                                                                                                                                                                              A,Molecule type: mRNA
A,Residues: 1-4,'L',6-32,'G',34-52,'E',54-73,'K',75-97 <RAW>
A,Residues: 1-4,'L',6-32,'G',34-52,'E',54-73,'K',75-97 <RAW>
A,Cross-references: EMBL:X62965
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
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S78486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Experimental source: clone FL13-28
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H) 3 genes and A;Reference number: S31104; MUID:92111633; PMID:1730252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S78486;
R;Raaphorst, F.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region (clone FL13-28) - human (fi C;Species: Homo sapiens (man) C;Date: 30-Apr-1998 #sequence revision 08-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, A, Reference number: $78486
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A; Residues: 1-114 < GRI>
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                                                                                                                                                                                                                                                                                                          F;15-98/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-117 <RAA>
A;Cross-references: EMBL:X62965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: S78486
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C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S31115
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                                                                       1 NIKQDGSEKYYADSVRG
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15; Conserv
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15; Conserv
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Pred. No.
                                                                                                                                                                                          Score 82; DB
Pred. No. 1.8
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RESULT 9
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A;Residues: 1-117 <KU2>
A;Cross-references: EMBL:X62128; NID:g38340; PIDN:CAA44059.1; PID:g38341
A;Note: the authors did not translate the codons for residues 6, 52, 54,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:Z14175; NID:g31015; PIDN:CAA78544.1; PID:g31016 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31675
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;31-114/Domain: immunoglobulin homology <IMM>
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R;Cuisinier, A.M.;
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                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-136 < CUI>
                                                                                                                                                                                                                                                                                        A; Reference number: S31585
A; Accession: S31587
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                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                             A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region - human
C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
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                                1 NIKODGSEKYYADSVRG 17
                                                                         l Similarity
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  NIKODGSEKYYVDSVKG
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88.2%;
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                                                                                         Score 82;
Pred. No.
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Pred. No.
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Pred. No.
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                                                                                                             Length 136;
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R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M. Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: 137781
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137781
                                                                                                               C;Accession: S31509

R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A;Description: Dominance of clonotypic patterns and variable
                                                                                                                                                                                                        Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
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S31509
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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Nucleic Acids Res. 20, 2601, 1992
A;Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a A;Reference number: S22657; MUID:92285150; PMID:1598223
A;Accession: S22657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain precursor V region (0-81VH) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 06-Feb-1998
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C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37781; S25475
                                                                  A; Reference number: S31509
A; Accession: S31509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;1-19/Domain: signal sequence #status predicted F;20-140/Product: Ig heavy chain (fragment) #stat F;34-117/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-140 <HIR>
A; Molecule type: mRNA
A; Residues: 1-123 < CHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Keywords: heterotetramer; immunoglobulin
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88.2%;
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;Cross-references: EMBL:X69864; NID:g33090; PIDN:CAA49498.1; PID:g33091

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Ig heavy-chain variable region (clone WHR) precursor - human (fragment) C;Species: Homo sapiens (man) C;Jate: 20-Jul-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000 C;Aacession: S60296 R;Kueppers, R.; Fischer, U.; Rajewsky, K.; Gause, A. Immunol. Lett. 34, 57-62, 1992 A;Title: Immunoglobulin heavy and light chain gene sequences of a human CD5 A;Reference number: S60295; MUID:93122853; PMID:1282498 A;Accession: S60295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, September 1991
A,Reference number: S16847
A,Accession: S16847
A,Status: preliminary
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                                                                              RESULT 15
S29543
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S60296
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S16847
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C;Superfamily: immunoglobulin region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
E;34-117/Domain: immunoglobulin homology <IMM>
Ig heavy chain V region (COS 3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C;Accession: S29543
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A; Residues: 1-136 < KUE>
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A;Molecule type: DNA
A;Residues: 1-136 <KUE>
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Local Similarity 82.4%;
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70 VKDDGSERYYVDSVKG 85
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Pred. No. 1.3e-05;
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Pred. No. 0.00072;
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R;Tomlinson, M.; Walter, G.; Cook, G.P.; Winter, G. submitted to the EMBL Data Library, October 1992
A;Reference number: S29543
A;Recession: S29543
A;Molecule type: DNA
A;Residues: 1-98 <TOM>
A;Coss.references: EMBL:Z17389; NID:g32835; PIDN:CAA78994.1; PID:g32836
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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51 IRYDGSNKYYADSVKG 66
                                                                                12;
                         2 IKQDGSEKYYADSVRG 17
                                                                                                      Similarity
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                                                                                                    74.2%; Score 66; DB 2; 75.0%; Pred. No. 0.00074;
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Search completed: January 12, 2004, 07:02:57 Job time : 15.4062 BECB

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2004, 06:47:49; Search time 9.29688 Seconds (without alignments) 85.992 Million cell updates/sec

Title: Perfect score: Sequence: US-09-829-495-62 89

1 NIKQDGSEKYYADSVRG 17

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

33333 3009	116 117 119 120 220 221 232 242 253	7 9 11 12 13 14	Result No. 2
41 41 41 40.5	44444444444444444444444444444444444444	D 50 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	SCOTE 53
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Q63632 rattus norv Q9uhw9 homo sapien Q924n4 mus musculu P40803 bacillus su P18358 staphylococ		P01774 homo sapien P01775 homo sapien P01770 homo sapien P01762 homo sapien P01762 homo sapien P01763 homo sapien P01763 homo sapien P01771 homo sapien P1810 carassius a P01771 homo sapien P18528 mus musculu P19181 carassius a	homo homo homo homo

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# ALIGNMENTS

RESULT 2 HV3G_HUMAN ID HV3G HUMAN STANDARD; PRT; 122 AA. AC P01758;	Qy 1 NIKQDGSEKYYADSVRG 17    ::  ::	Query Match 70.8%; Score 63; DB 1; Length 116; Best Local Similarity 58.8%; Pred. No. 0.00088; Matches 10; Conservative 5; Mismatches 2; Indels 0;	RESULT 1  FY3T HUMAN  ID HV3T HUMAN  AC P01781;  DT 21-UTL-1986 (Rel. 01, Created)  DT 21-UTL-1986 (Rel. 02, Last annotation update)  DT 21-UTL-1986 (Rel. 02, Last annotation update)  DT 15-SEP-2003 (Rel. 42, Last annotation update)  DT 15-SEP-2003 (Rel. 42, Last annotation update)  DE 19 heavy chain V.III region GAL.  OS Homo sapiens (Human).  OC Mammalia; Entheria; Primates; Catarrhini; Hominidae; Homo.  OX MCBI_TaxID=9606;  RN [1]  RR SEQUENCE.  RR MEDILINE-75059123; PubMed=4803843;  RA MALLINE-75059123; PubMed=4803843;  RA MALLINE-75059123; PubMed=4803843;  RA MEDILINE-75059123; PubMed=4803843;  RA Hilschmann N.;  RI Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).  RA HILSCHLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.  CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.  DR PIR; A02064, MSHUGL.  DR GO; GO:000393; F:antigen binding activity; NAS.  DR GO; GO:000595; P:immune response; NAS.  DR GO; GO:0004933; F:antigen binding activity; NAS.  DR GO; GO:0004935; P:immune response; NAS.  DR GO; GO:000406; IGv; 1.  DR PROSITE; PRO03106; Ig-MiC.  DR FIRM; FFOOD THO 110; IG-LIKE; 1.  DR PROSITE; PS0835; Id LIKE; 1.  PROSITE; PS0835; Id	
		0; Gaps 0;	leostomi;  ann N.;  1 nolecule.";	

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GO; GO:0003823; F:antigen bindi
GO; GO:0006955; P:immune respor
InterPro; IPR007110; Ig-like.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
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21-JUL-1986 (Rel. 01,
15-SEP-2003 (Rel. 42,
Ig heavy chain V-III r
Homo sapiens (Human)
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
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"Amino acid sequence of the variable region of a location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3339-3243(1980)
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FR
                                                                         Eur. J Biochem. 228:886-893(1995).

1: SINILARITY: Contains 1 immunoglobulin-lipIR; 869132, 869132.

HSSP; P01810; 2FBJ.

GO; GO:00005976; C:extracellular; NAS.

GO; GO:0001823; F:antigen binding activity;

GO; GO:00005955; P:immune response; NAS.
                                                                                                                                                                                                       MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A.,
"Characterization of the two unique
immunglobulins.";
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P80419;
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PROSITE; PS50835; IG LIKE;
Immunoglobulin V region; Py
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Lehman D.W., Putnam F.W.;
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122 AA;
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ain V-III region GAR.
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HSSP; P01772; 2FB4.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding activity; NA
G0; G0:000823; F:antigen binding activity; NA
G0; G0:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_wHC.
InterPro; IPR003396; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Glycoprotein; Pyrroli
Immunoglobulin V region; Glycoprotein; Pyrroli
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PROSITE; PS50835; IG LIKE; 1
Immunoglobulin V region.
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MEDLINE=79151016; PubMed=107164;

Putnam F.W., Liu Y.-S.V., Low T.L.K.;

"Primary structure of a human IgA1 immunoglobulin. I

"BA1 protease, digestion, Fab and Fc fragments, and

amino acid sequence of the alpha 1 heavy chain.";

J. Biol. Chem. 254:2865-2874(1979).

J. BIOL. Chem. 254:2865-2874(1979).
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P01773;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

15-SEP-2003 (Rel. 42, Last annotation

Ig heavy chain V-III region BUR.
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Mammalia; Eutheria;
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InterPro; IPR003006; Ig MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                        SEQUENCE
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.0-A resolution."
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51
                                    10;
                  N
                                              Similarity
                 IKODGSEKYYADSVRG 17
                                                                                                                                                                                                                                                                                                                                                        PS50835;
IWDDGSDQHYADSVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                        AA;
                                                                                                                                                                                                                                                                                                                                    V region;
                                                                                                                                                                                                                                                                                                                                                       IG LIKE;
                                                                                                                                                                                                                                                                                      96
110
7
12
                                           61.8%;
                                                                        13718 MW;
                                                                                                                                                                                                                                                                                                                                    3D-structure; Pyrrolidone carboxylic IG-LIKE.
66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin-like domain
                                   4;
                                            Score 55;
Pred. No.
                                                                                                                                                                                                                                                                                                                          PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                       E4D71B52B16F8776 CRC64;
                                   Mismatches
                                            DB 1;
0.022;
                                   <u>ب</u>
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                                                   Length 126
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RESULT

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RESULT
HV3N_H
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  Query Match
Best Local S
Matches 8
                               Capra JD., Kehoe J.M.,
Capra JD., Kehoe J.M.,
Structure of antibodies with shared
of the heavy chain variable regions
anti-gamma globulins ",
proc. Natl. Acad. Sci. U.S.A. 71:403
                                                                                                                                                                                                                                                                                                                                                 HV3N HUMAN STA
P01775;
21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
15-SEP-2003 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
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G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding activ
G0; G0:0003825; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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P01774;
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                                                                                                                                                                       SEQUENCE.
MEDLINE=75046755;
                                                                                                                                                                                                                         NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-gamma globulins.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Capra J.D., Kehoe J.M.;
"Structure of antibodies with shared idiotypy:
"Anain variable regions of two immu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606; [1]
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
15 heavy chain V-III region LAY.
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MISCELLANEOUS: TH
GLOBULIN ACTIVITY
SIMILARITY: Conta
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el. 42, Last annotation
LV-III region POM.
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Contains 1 immunoglobulin-like domain
                                                                                                                                                   PubMed=4139708;
J.M.;
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01, Last seq
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57.1%;
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N -> D (PROBABLY DUE TOURING ISOLATION).

/FTId=VAR_003966.
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Pred. No. 0.
                                                                                                        shared idiotypy:
egions of two imm
                                           71:4032-4036(1974)
WAS ISOLATED FROM
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RESULT
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Best Local S
Matches 8
InterPro; Iran-

InterPro; Iran-

Pfam; PF00047; 19; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

Immunoglobulin V region; PyrroLIDONE CARBOXYLIC
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21-JUL-1986
15-SEP-2003
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activ
GO; GO:0003823; F:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003306; Ig_V.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE;
Immunoglobulin V region.
                                                                                                                                                       HSSP; P01772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.

GO; GO:0003823; F:antigen binding activity; NAS.

GO; GO:0006555; P:immune response; NAS.
                                                                                                                                                                                                                                                            Dreker L., Schwarz J., Reichel W., Hilschmann N.;
"Rule of antibody structure. The primary Structure of a monoclonal
IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
characterization of the protein, the L- and H-chains, the
cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
-i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                         Ponstingl H., Hilschmann N.;

"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.
MEDLINE=77070269; PubMed=826475;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens (Human)
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P01770;
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                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=77070267; PubMed=1002129;
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                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                DISULFIDE BOND
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8; Conserv
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986 (Rel. 01, Last sequence update)
9003 (Rel. 42, Last annotation update)
chain V-III region NIE.
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119
119 AA;
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larity 57.1%;
Conservative
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Pred. No. 0.15
5; Mismatches
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                           PYRROLIDONE CARBOXYLIC ACID
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                                                                                                                                                                                                                                    domain
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RESULT
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Matches 9
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                                                           HHUMAN
HVJSH HUMAN
STANDARD;
P01769;
P017796 (Rel. 01, Created 21-JUL-1986 (Rel. 01, Last set 15-SEP-2003 (Rel. 42, Last and 15 heavy chain V-III region G. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; lrxvvv.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

Immunoglobulin V region; Pyrrolidone Carboxylic ACID.

1 108 PYRROLIDONE CARBOXYLIC ACID.
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HV3A HUMAN
P01762;
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           II. The amino acid sequence or the complete IgA-molecule.";
structure of the complete IgA-molecule.";
hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
-i- MISCELLANEOUS: THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
-i- STMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON TER
SEQUENCE
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A02045; A1HUTR.
HSSP; P01772; 2FB4.
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MEDLINE=76023781; PubMed=809331;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kratzin H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986
15-SEP-2003
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The primary structure of a monoclonal IgA-
The primary structure of the H-chain,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        Similarity 9; Conserv
                                                                                                                                                                                                                                                                                                                                                GSEKYYADSVRG
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(Rel. 42, Last annotation
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61.5%;
                          Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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75.0%;
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Last annotation 
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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subgroup II
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HV3B_HUMAN
PIR; A02149; Name PIR; A02149; Name PIR; A02149; Name PIR; PO1772; 2FB4.

GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-ilke.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
INTERPRO; IPR003596; Ig_v.
R Pfam; PF00047; Ig; 1.
R PROSITE; PS00406; IGv; 1.
R PROSITE; PS50835; IG LIKE; 1.
IMMUNOGIOBULIN VEGION; PYTROLIDONE CARBOXYLIC ACII
FT DOMAIN
1 112 PYRROLIDONE CARBOXYLIC ACII
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Best Local S
Matches 8
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21-JUL-1986
15-SEP-2003
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NON_TER
SEQUENCE
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"The switch point in mu heavy chains of human IgM immunoglobulins.";
Biochemistry 13:2482-2498(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE
                                                                                                                                                                                                                                                    (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsiella polysaccharides K30 and K33."; proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A02052; M3HUGA.
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P01763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HV3B
                                                                                                                                                                                                                -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                          Goni F., Frangione B.; "Amino acid sequence of the Fv region of a human monoclonal
                                                                                                                                                                                                                                                                                                                                       MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=74175307; PubMed=4208843;
Florent G., Lehman D., Putnam F.W
                                                                                                                                                                                                                                                                                                                                                                                                                                  g heavy chain V-III region
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GO:0003823; F:antigen binding activity; NAS
GO:0006555; P:immune response; NAS.
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                                                                                                                                                                                                                            WALDENSTROM'S MACROGLOBULINEMIA
                                                                                                                                                                                                                                         AGAINST 3,4-PYRUVYLATED GALACTOSE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMAN
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122
122 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 01, Created)
(Rel. 01, Last seq
(Rel. 42, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                               01, Last sequence update)
42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
13166 MW;
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50.0%;
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Pred.
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                         PYRROLIDONE CARBOXYLIC ACID
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No.
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RESULT 12
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NON TER
SEQUENCE
                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region 3 precursor. Carassius auratus (Goldfish). Garassius auratus (Goldfish). Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii, Neopterygii, Teleostei, Ostariophysi; Cypriniformes; Cyprinidae; Carassius.
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                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson M.R., Middleton D., Warr G.W.; "Immunoglobulin heavy chain variable region and family relationships of two genes and a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                           PIR; A28966; A28966.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P19180;
                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                      Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                  EMBL; J03616; AAA50807.1;
                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                       [nterPro;
                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                          ish."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDLINE=88144476; PubMed=3125551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICBI_TaxID=7957
                                                                                                                                                                                                  mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE FROM N.A.
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9; Conserv
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                                                     Similarity
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                                                                                                                                                                                                            PS50835;
IYDDGSDVSYADTVKG
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                     56.2%;
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75.0%;
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85
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Pred. No.
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COMPLEMENTARITY-DETERMINING-2
FRAMEWORK-3.
                                                                                                                                                    IG HEAVY CHAIN V REGION 3. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
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                                                               DB 1;
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pseudogene in a
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RESULT 13

HV3J_HUMAN

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RESULT 14
HV57_MOUSE
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    DR DR RETT
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Best Local S
Matches
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NON_TER
SEQUENCE
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Biochemistry 18:553-560(1979)
                    PIR; JT0501; HVMS96.
HSSP; P01772; 2FB4.
InterPro; IPR007110;
                                                                                 MEDIINE-89279149; PubMed-2499654;
Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.
"Barly onset of somatic mutation in immunoglobulin VH g
the primary immune response.";
J. Exp. Med. 169:2007-2019(1999).
-!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183
-!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel.
01-NOV-1990 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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PIR; A02054; G1HUHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chiu Y.-Y.H., Lopez de Castro J.A., Poljak R.J.; "Amino acid sequence of the VH region of human myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=79124695; PubMed=420800;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Last seque)
15-SEP-2003 (Rel. 42, Last annot)
15 heavy chain V-III region HIL.
Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
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P18528;
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                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=BALB/CJ;
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10090;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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bulin V region; Pyrrolidone carboxylic acid
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121 AA;
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42, Last annotation
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Rodentia;
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Ig-like.
Ig_MHC.
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61.5%;
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Pred. No. 0.
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VH genes
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DOMAIN 1
NON_TER 98
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SMART; SM00406; IGv; 1
SMART; SM00406; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                        DISULFID NON TER SEQUENCE
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                                                                                                                                                    SIGNAL
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Eukaryota, Metazoa, Chordata, Craniata, Actinopterygii, Neopterygii; Teleostei; Cyprinidae, Carassius.
                                                                                                               DOMAIN.
                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                 Wilson M.R., Middleton D., Warr G.W.; "Immunoglobulin heavy chain variable region gene evolution: and family relationships of two genes and a pseudogene in a
                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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Wilson M.R., Middleton D., Warr G
"Immunoglobulin heavy chain varia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                        fish."
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                           FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
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                                       Pred. No. 1;
                                                        Score 45;
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0.87;
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Ostariophysi; Cypriniformes;
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Search completed: January Job time: 10.2969 secs

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Result
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Listing first 45 summaries
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47.5
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1: sp_archea:*
2: sp_bacteria
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sp_phage:*
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sp_virus:*
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Q9ulb6 homo sapien
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Q9ul93 homo sapien
Q9ul84 homo sapien
Q9ul84 homo sapien
Q9ul71 homo sapien
Q9uf71 salmo trutt
Q8nc16 homo sapien
Q9uf72 homo sapien
Q9uf72 homo sapien
Q9uf74 rickettsia
Q9rzy6 drosophila
Q9f5k2 rhizobium t
Q98f04 rhizobium 1
Q96bb9 homo sapien
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Q812S2 Q81538 Q9GJ66
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## ALIGNMENTS

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MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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MEDLINE-98277139; Van der Merwe P.L.,
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InterPro; IPR007110;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                           fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035021; AAD56257.1; -.
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Mammalia; Eutheria;
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InterPro; IPR003006; Ig_MHC.
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Submitted (DEC-2001) to the EMB Submitted (DEC-2001);
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
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Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
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                 Clin. Immunol. Immunopathol.
EMBL; AF035030; AAD56266.1; -
HSSP; P01772; 2FB4.
InterPro; IPR007110; Ig-like.
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MEDLINE=98277139; PubMed=9614934;

MEDLINE=98277139; PubMed=9614934;
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"Myosin-reactive autoantibodies
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Pred.
                                                                            87:184-192(1998)
                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                      Kalis
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                                                                                                                   rheumatic
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                                                                                                                                                      N.N.,
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                                                                                                                   carditis
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                                                                                                                                                        Berney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRC64;
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                                                                                                                                                        S.M.
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RESULT
Q9Y509
ID Q9Y509
AC Q9
AC Q9
DT 01
DT 01
DT 01
DT VH
GN VH
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Q9UL71
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Best Local Similarity
Matches 11; Conser
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 10; Conserv
Eukaryota; Metazoa; C
Mammalia; Eutheria; E
NCBI_TaxID=9606;
[1]
                                                                                                                      01-NOV-1999
01-MAR-2003
VH3 protein
                                                                                                                                                                                                    Q9Y509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9UL71;
Q9UL71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; ig; 1. —
SMART; SM00406; IG-; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLLINE=98277139; PubMed=9614934;

Mu X., Liu B., Van der Merwe P.L.,

Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01.MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG LIKE;

NON TER 1 1 1

NON TER 122 122
                                                                                                                                                                                   01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF035043; AAI
HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Young D.C.; "Myosin-reactive autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like,
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003596; Ig_v.
                                                                            iomo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fragment)
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                                                                                                                    protein
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122 AA;
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121 AA;
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(TrEMBLrel.
(TrEMBLrel.
(Fragment).
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                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
13154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13579 MW;
                                        Primates;
                                                         Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                             59.6%;
62.5%;
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12,
23,
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                                                                                                                                       , Created)
, Last sequence up
, Last annotation :
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87:184-192(1998).
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Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                      Catarrhini;
                                                           Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2F045CCFA5D50736 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
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                                        Hominidae; Homo
                                                                                                                                                              update)
                                                                                                                                       update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 121;
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RESULT 9
Q8NCL6
ID Q8NC
AC Q8NC
DT 01-C
DT 01-C
DT 01-W
DE Hypo
OS Homo
OC Euka
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Q9GJ71
ID Q9
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Best Local S
Matches 8
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Best Local S
Matches 10
                                                QBNCL6;
QBNCL6;
01-OCT-2002
01-OCT-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9GJ71
Q9GJ71;
01-MAR-2001
                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
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MEDLINE=96071149; PubMed=7475288;

Cao J. Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee
Lichtenstein A.K., Berenson J.R.;

"A CD10-positive subset of malignant cells is identified
"A CD10-positive subset of malignant cells is identified."
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ90170.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                        Stet R.J.M., Jordan W.C.;

"Class II alpha chain in brown trout (Salmo trutta).";

"Ulass II alpha chain in brown trout (Salmo trutta).";

"Submitted (SEP-2000) to the EMBL/GenBank/DDBJ database;

EMBL; AJ293950; CAC08187.1;

InterPro; IPR001003; MHC_II_alpha.

Pfam; PF00993; MHC_II_alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmo trutta (Brown trout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC class II alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myeloma using PCR with patient-specific immunoglobulin gene primers."; Leukemia 9:1948-1953(1995).
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=8032;
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                                                                                                                                                                                                                    8; Conserv
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                                                                                                                                                                                             DGSEKYYADSVRG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISYDGSTQYYAGSVKG
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                                                                                                                                                                    DGEEKWYADFIKG
                                                                                                                                                                                                                                                                      71
71 AA;
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                                                                                                                                                                                                                     Conservative
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                     7699 MW;
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                                                                                                                                                                                                                                56.2%;
61.5%;
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Pred. No.
                                                                                                                                                                                                                                Score 50; I
Pred. No. 0.
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                                                                                                     PRT;
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                                                                                                     493
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0.97;
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InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PP00047; Ig; 4.
SMART; SM00409; IG; 4.
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TISSUE-Mammary gland;
IIGGAI T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugai K., Sugano S., Ishii S., Kawai-Hio Y., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Suzuki Y., Nagai K., Sugano S., Ishii S., Kojima S., Nagahi Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahi Yamamoto J., Wakamatsu A., Yoshikawa Y., Aotsuka S., S. Hattori A., Okumura K., Imayanagi T., Ninomiya K.;
"NEDO human cDNA sequencing project.";
"NEDO human cDNA sequencing project.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=98277139; PubMed=9614934;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
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Mammalia; Eutheria; Primates;
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Pred. No.
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STRAIN-Madrid E;
MEDLINE-99039499; PubMed-9823893;
MEDLINE-99039499; PubMed-9823893;
Andersson S.G.E., Zomorodipour A., Anders
A Sicheritz-Ponten T., Alemark U.C.M., Pod-
A Sicheritz-Ponten T., Minkler H.H., Kurland C.
A Eriksson A.-S., Winkler H.H., Kurland C.
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01-DEC-2001
01-JUN-2002
 01-MAY-1999
01-MAY-1999
01-JUN-2002
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 Samson D., Roux V., Raoult D.;
Complete
SEQUENCE
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 MEDLINE=21442074; PubMed=11557893;
Ogata H., Audic S., Renesto-Audiffren P., Rosmson D., Roux V., Cossart P., Weissenbach
 EMBL; AJ235272; CAA15013.1; -.
InterPro; IPR005311; PBP_dimer.
InterPro; IPR001460; Transpeptdse.
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InterPro; IPR001460; Transpeptdse
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 Penicillin-binding protein. PBPA1 OR RC0852.
 Rickettsiaceae;
NCBI_TaxID=782;
 01-MAY 1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-JUN-2002 (TrEMBLrel. 21, Penicillin-binding protein
 Science
 Rickettsia conorii.
 mitochondria."
 Bacteria; Proteobacteria;
 Rickettsia prowazekii.
 Nature 396:133-140(1998).
 Mechanisms of evolution in Rickettsia conorii science 293:2093-2098(2001).
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 NIGKSGIEKYYDNKLRG 210
 NIKODGSEKYYADSVRG 17
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 Matches
 Banzon J.,
Carlson J.,
Dodson K.,
 01-MAY-2000
01-OCT-2002
 Q9VZF9; Q8SZQ3;
 Drosophila melanogaster (Fruit
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Celniker S.E., Adams M.D.,
Evans C.A., Gocayne J.D.,
 MEDLINE=20196006; PubMed=10731132;
 SEQUENCE FROM N
 NCBI_TaxID=7227;
 Sphydroidea; Drosophilidae;
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 protein
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, Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y
An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.
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Hradecky P., Huang Y., F
Tupy J.L., Bergman C., E
Clamp M., Drysdale R., E
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Q1-MAR-2001
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01-MAR-2003
 George R., Chavez C., Dorsett V., Dresnek D., Farfan D., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., 1 Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Patel S., Phouanenavong S., Wan K., Yu C., Lewis Celniker S.;
 SEQUENCE FROM N.A.
Adams M.D., Celniker
Submitted (MAR-2000)
 Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco : Pacleb J., Paragas V., Park S., Patel S., Péléffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F. Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M., "Sequencing of Drosophila melanogaster genome.", submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 PRINTS; PR00947; CUTICLE. -
PROSITE; PS00233; CUTICLE; 1.
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 Probable ABC-transporter
 Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis "Annotation of Drosophila melanogaster genome."; Submitted (WAR-2000) to the EMBL/GenBank/DDBJ databases.
 Kronmiller B., Marshall B., Millburn G., Richter J., Rus
Searle S.M.J., Smith B., Shu S., Smutniak F., Whitfield
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 FlyBase;
 SEQUENCE FROM
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 179
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A WALANADE A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
A Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Watsuno A.,
A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti.";
AL Mesorhizobium loti.";
BMA Res. 7:331-336(2000).
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"ORF 342, a potential binding protein of an ABC transporter in Rhizobium tropici CIAT 899.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF317885; AAG31660.1; -.
InterPro; IPR006059; SBP_bac_1.
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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MEDLINE=21082930; PubMed=11214968;
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294 GAEKYYSDEMKG 305
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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1998.DAT:*
 /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
 /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
 /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
 17
17
17
98
98
98
98
 BB
 Gapext 0.5
 Ħ
 AAB61294
ABU11260
AAO17611
AAR52066
AAR72074
AAB40138
AAB40140
ABG91901
ABG78210
 SUMMARIES
 1107863
Human FAPalpha spe
Heavy chain variab
DP54 VH region. H
Anti-hIL12 antibod
Anti-hIL12 antibod
Human antibody fra
Human Fv molecule
 Description
 Anti-TANGO 268 scF
Human TANGO 268 VH
 . DAT: *
```

Anti-hIL-12 antibo	AAB39487	21	17	74.2	66
Human BLyS binding	ABP45806	23	249	75.3	67
Human HIV-1 monocl	AAB62778	22	123	•	67
anti-Rh(D)	AAG93629	22	117	•	67
Anti-hIL12 antibod	AAB39822	21	17		67
immun	AAR66340	16	116	٠	69
Anti-hIL12 antibod	86	21	17	٠	69
_	AAW24537	18	130	79.8	71
CDR #2 of r101-2 h	AAW24547	18	17	•	71
Anti-hIL12 antibod	AAB39824	21	17	•	72
Human BLyS binding	ABP45339	23	254		73
Tumour antigen ant	AAY05055	20	17	•	73
Human BLyS binding	ABP45500	23	254		74
ъ.	AAU75745	23	122	•	74
BLys	47	23	250		75
Human BLyS binding	ABP45308	23	250	•	75
₫	AAY05049	20	17	•	75
Protein for clone	AAU75154	23	265	•	76
for	AAU75153	23	265	٠	76
Amino acid sequenc	AAU75149	23	265	٠	76
Protein for affini	AAU75152	23	264	٠	76
anti-	AAU75737	23	122	•	78
(CP) -1	AAU75740	23	17	•	78
Single chain antib	ABG74385	24	312	92.1	82
	ABB09604	23	312	•	82
Single chain Apo-2	AAW83323	20	312	•	82
clon	AAW90180	20	271	•	82
Anti-FAPalpha anti	AAO14058	23	262	•	82
	499	23	253	•	82
Human BLyS binding	ABP44992	23	253		82
	ABP45583	23	251	•	82
	ABP45459	23	247	•	82
BLyS	ABP45878	23	241	•	82
anti-	404	23	134	•	82
HIV-1	27	22	125	92.1	82
Human immunoglobul	AAR66301	16	-	92.1	82

## ALIGNMENTS

RESULT 1
AAB61294
IID AAB6
XX AAB62
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XX AAB6
XX Huna
XX Huna
XX Huna
XX TANG
XX OLOC
XX Human; antibody; scFv; CDR; complementarity determining region; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; s 30-JUN-1999; 06-DEC-1999; 04-APR-2001 AAB61294; AAB61294 standard; 30-JUN-2000; 2000WO-US18152. 04-JAN-2001. WO200100810-A1. Homo sapiens. cancer Anti-TANGO 268 scFv CDR, SEQ 14-FEB-2000; ischaemia; cardiovascular disease; (MILL-) MILLENNIUM PHARM INC 99US-0345468. 99US-0454824. 2000US-0503387. (first entry) Peptide; 17 ID NO: B disorder; haemorrhagic disorder; stroke;
se; immunological disease; liver disorder; 62.

GPVI;

```
ABU11260
ID ABU1
XX
AC ABU1
XX
DE Huma
XX
Hog
XX
Hog
XX
Hog
XX
Hog
XX
Hom
Core
XX

 밁
 Ś
 RESULT
 Best
 Matches
 Query Match
 Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein.VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboenbolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; angina pectoris; myocardial infarction; cardiovascular disease; angina pectoris; myocardial infarction; coronary restenosis; atherosclerosis; immunological disorder; developmental disorder; embryonic disorder; liver disorder; cerebral vascular disease; venous thromboembolism disease.
 ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombotytopaenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent acture cardiac ischaemia following angioplasty and metastatic cancers, especially of the colon and liver.
 Busfield SJ, v....
MD, Kingsbury
 The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,
 New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and
 09-APR-2001; 2001US-0829495.
 09-APR-2002; 2002WO-US11122
 17-OCT-2002
 WO200280968-A1
 Homo sapiens.
 Human TANGO 268 VHCDR2 Peptide #3
 06-FEB-2003
 ABU11260;
 Sequence
 Claim
 and diagnosing hemorrhagic immunological disorders -
 ABU11260 standard; Peptide;
 (MILL-) MILLENNIUM PHARM INC
 Local
 31; Page 102;
 μ
 l Similarity
 NIKODGSEKYYADSVRG
 NIKODGSEKYYADSVRG
 17
 Conservative
 Villelal J,
 (first entry)
 A
K
 227pp; English.
 Ü
 100.0%;
 17
 Jandrot-Perrus M,
 17
 0
 Score 89; DB 22;
Pred. No. 2.9e-08;
; Mismatches 0;
 A
 Vainchencker W,
 Length 17;
 Indels
 0
 Gill DS;
 Gaps
 0
```

```
continuous specifically binding to a TANGO 268 (also referred as glycoprotein CC (immunospecifically binding to a TANGO 268) to a Collagen or platelet release of the invention act to decrease or CC collagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration, CC morphology, differentiation and/or function of megakaryocytes and CC platelets, including during development e.g. embryogenesis, modulating platelet, and including during development e.g. embryogenesis in CC leukocyte-platelet and platelet-endothelium interactions in CC migration. They are also useful for modulating platelet aggregation and CC with abnormal or aberrant megakaryocyte and/or platelet proliferation, CC migration, morphology, differentiation and/or function, e.g. bleeding CC disorders such as thrombocytopaenia. Other diseases which may be condulated by these antibodies are thrombotic disorders, cerebral CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism CC diseases including angina pectoris, myocardial infarction, coronary coronary coronary diseases, venous thromboembolism diseases, venous thromboembolism diseases, coronary diseases, venous thromboembolism diseases, coronary diseases, coronary diseases, venous thromboembolism diseases, coronary diseases, c
 variable heavy (VH) complementarity determining region (CDR)1, or VH CDR3, or variable light (VL) CDR1, VL CDR2 or VL CDR3, at immunospecifically binding to a TANGO 268 (also referred as gl) VI (GPVI)) antigen. The antibodies of the invention act to decivity (GPVI))
 Busfield SJ, Villey
Qian DM, Kingsbury
 This invention variable heavy
 Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 generate
 Claim
 7; Page 111; 236pp; English
 The present sequence represents a peptide sequence used to the antibodies of the invention.
 Villeval J,
 relates to
 a novel
 Jandrot-Perrus M,
 purified antibody comprising
 Vainchencker W,
 VH CDR2
 Gill DS
```

```
Query Match
Best Local S
Matches 17
 1 NIKODGSEKYYADSVRG 17
 17;
 Similarity
NIKODGSEKYYADSVRG
 Conservative
 100.0%;
17
 0,
 Score 89;
Pred. No.
 Mismatches
 2.9e-08;
 DB 24;
 0
 Length 17;
 Indels
 0
 Gaps
 0
```

```
RESULT 3
AAO17611
```

맑 Ś

Sequence

17

A

AAO17611 standard; Peptide;

AAO17611;

08-AUG-2002 (first entry)

Human FAPalpha specific VL region from VH50 CDR2 peptide

Human; FAPalpha; fibroblast activating protein alpha; antibody; Ab; gene therapy; cancer; wound healing; inflammation; cytostatic. therapy;

WO200168708-A2

20-SEP-2001.

16-MAR-2001; 2001WO-EP04716

```
RESULT 4
AAR52066
 밁
 S
 Query Match
Best Local S
Matches 15
 The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stromal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
 Park J,
Schmidt
 cancer, pancreatic cancer and metastatic brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a peptide described in the exemplification of the
 New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung or breast cancer
 Region
 antibody; humanised; murine; human; heavy chain; light; variable; framework region; complementarity determining region; reshaping; modelling; surface residue; modify.
 11-OCT-1996
 N-PSDB; AAL46556
 Region
 Region
 Region
 Heavy chain variable region of human PL0123 antibody.
 AAR52066 standard; Protein;
 Disclosure; Fig 6C; 109pp; English
 WPI; 2002-041180/05
 17-MAR-2000; 2000DE-1013286.
11-SEP-2000; 2000GB-0022216.
 EP592106-A1
 Homo sapiens
 invention
 (BOEH)
 Н
 1 NIKODGSEKYYADSVRG 17
 Similarity
 BOEHRINGER INGELHEIM PHARMA KG
 NIKQDGSEKYYVDSVKG 17
 Garin-Chesa P,
 17
 (first entry)
 Conservative
 A,
 /label= framework_region_1
/note= "FR 1"
 Location/Qualifiers
 /label= complementarity_determining_region_1
/note= "CDR 1"
 note=
 note=
 92.1%;
 "FR 2"
 "FR 3"
 "CDR 2"
 Pfizenmaier K,
 98
 Score 82; DB 23;
Pred. No. 4.5e-07;
 Mismatches
 Moosmayer D,
 Length 17,
 Indels
 Mersmann
 0;
 <u>.</u>
 Gaps
 0
```

```
RESULT 5
AAR7207
AAR7207
XX AAR7
XX AAR7
XX AAR7
XX AAR7
XX AAR7
XX Grav
DT 25-M
DT 26-S
XX Grav
CH
DE DP54
XX Grav
XX Homo
XX Homo
XX Homo
XX Key
FT Regi
FT Regi
FT Regi
FT Regi
XX WO95
XX WO95
XX WO95
XX SO-M
PD 30-M
XX PF 22-S
XX PF 22-S
 밁
 Ś
 Query Match
Best Local S
Matches 15
 Modification of a rodent antibody (Ab) or fragment by resurfacing in order to produce a humanised rodent Ab can be determined by calculating homology between murine and human Ab antibody surfaces. In order to test the resurfacing approach of the invention, three humanisation experiments were set up: (1) traditional loop grafting; (2) resurfacing approach using most similar chain; and (3) resurfacing approach using human sequences with most similar surface residues. The Ab used was the murine anti-N901 Ab (see AAR52061). Experiment 3 was carried out using the present sequence which represents the human PiO123 Ab light chain variable region with 74 percent homology with anti-N901 Ab. N901/PIO123 (AAR52067) was prepd. by resurfacing. Sequence numbering starts at possition 118 in the specification.
 Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H cha
 Method of resurfacing of rodent antibodies to produce humanised antibody forms - for producing non-human antibodies with improved therapeutic efficiency by presenting human surface on V-region
 DP54 VH region.
 25-MAR-2003
26-SEP-1995
 AAR72074;
 AAR72074 standard; Protein; 98
 Sequence
 Guild BC,
 22-SEP-1993;
 22-SEP-1994;
 30-MAR-1995.
 WO9508336-A1
 Region
 Region
 Homo sapiens.
 variable region; autoimmunity.
 Example 1; Fig
 WPI; 1994-120230/15.
 09-SEP-1992;
 13-APR-1994
 (IMMU-) IMMUNOGEN INC.
 (PEDE/) PEDERSEN J T.
 50 NIKODGSEKYYVDSVKG
 15;
 1 NIKODGSEKYYADSVRG
 Similarity
 98 AA;
 Pedersen JT,
 Conservative
 (updated)
(first entry)
 4B; 230pp; English
 92US-0942245
 93US-0124469
 94WO-US10756
 /label= CDR1
49..67
/label= CDR2
 93EP-0307051.
 Location/Qualifiers
 92.1%;
88.2%;
 Rees
 66
 17
 Score 82;
Pred. No. 3
 ₽Ŗ,
 B
 Mismatches
 Roguska MA,
 DB 15;
 .4e-06;
 Length 98
 Searle
 Indels
 H chain;
 SMJ;
 0
 Gaps
```

0;

```
RESULT 6
AAB40138
ID AAB4
XX A
 밁
 δ
 Query Match
Best Local
 Matches
 Salfeld JG, Koyu....
Kaymakcalan Z, Labkovs
GM, Venturini
 New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohi disease and multiple sclerosis -
 complementarity determining region; CDR; antirheumatic; antiarrhritic; antisclerotic; neuroprotective; antipsoriatic; antiasthmatic; cardiant; antiparasitic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis.
 05-FEB-2001
 Sequence
 OF7H1.19, are provided
 showed
 tissue
 L- and
 Disclosure;
 by molecular cloning
 N-PSDB;
 WPI; 1995-139383/18.
 AAB40138
 25-MAR-1999;
 Human; neutralising antibody; interleukin-12; IL-12; antiinflammatory;
 Anti-hIL12 antibody H chain V region amino acid sequence
 24-MAR-2000; 2000WO-US07946.
 (Updated
 fragments were obtained.
 (NICH-) NICHOLS INST DIAGNOSTICS
 and H-chain DNA was amplified by PCR from Graves' orbital sue and clones encoding autoimmune-associated immunoglobulin gments were obtained. 2/15 clones of H chain (IgGl) genes wed homology to the germline gene DP54 (AAQ89332), which encodes protein given in AAR72074. The DNA (AAQ89333) and corresp. amino d (AAR72075) sequences of the VH region of a representative clone,
 sapiens
 50
 _
 l Similarity
15; Conser
 ophthalmopathy-associated monoclonal
 BASF AG.
GENETICS INST INC.
 standard;
 NIKODGSEKYYADSVRG
 NIKQDGSEKYYVDSVKG
 g
 SM.
 , Roguska M, ra. Z, Labkovsky B, San. Trini A, Warne NW
 된,
 86
 25-MAR-2003
 Page 72; 94pp;
 Conservative
 (first entry)
 Æ;
 9908-0126603
 Protein;
 92.1%;
 얁
 to correct PN field.)
 immunoglobulin
 Paskind M, Banerjee S, Tracey DE, White M;
cy B, Sakorafas P, Friedrich S, Myles A;
A, Warne NM, Widom A, Elvin JG, Duncan AR;
S, Smith S, Holtet TL, Du Fou SL;
 17
 99
 English.
 1;
 Score 82; DB Pred. No. 3.4e
1; Mismatches
 3.4e-06;
 genes
 antibody -
 Length 98;
 Indels
 produced
 SEQ ID
 e.g. Crohn's
 0
 Gaps
 amino
 0
```

```
CC anti-II-12 antibody heavy and light chain complementarity determining cregion (CDR) amino acid sequences, and also includes variable region complementarity determining cregion (CDR) amino acid sequences. Other variable region amino acid sequences are complementarity and provided sequences are complementarity. Sequences ABB39517-B39510 and ABB40068-B40149. Sequences ABB39518-B39771 compresent other CDR3 related amino acid sequences, AAB39772-B40063 compensus sequences are given in ABB40064-B40067. Primers used in the identification and comparative in ABB40064-B40067. Primers used in the identification and comparative in ABB40062-C61071. The antibodies of the invention are given in ABB40062-C61071. The antibody of the invention is a neutralising complementary; neuroprotective; antiarthritic; antiarthratic; antiarthmatic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. CC cardiant; antiparasitic; antibacterial and immunosuppressive activity. CC despecially Crohn's disease, multiple sclerosis and rheumatoid arthritis. CC They can also be used in the manufacture of a pharmaceutical composition and alcordary.
 This invention relates to a new human antibody specific for human interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent hu
 Claim
 75; Page 122;
 human IL-12 disorders.
 98
 AA,
 377pp; English.
 human
```

```
Query Match
Best Local S
50
 1 NIKODGSEKYYADSVRG
 Similarity
15; Conserv
NIKODGSEKYYVDSVKG
 Conservative
 92.1%;
88.2%;
66
 17
 Score
Pred.
 Mismatches
 No.
 ; DB 21;
. 3.4e-06;
 Length
 Indels
 0
 Gaps
 0
```

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Ş

RESULT 7 AAB40140 ID AAB4 05-FEB-2001 AAB40140 standard; Protein; (first entry) 98

complementarity determining region; CDR; antirheumatic; antiarthritic; antisclerotic; neuroprotective; antipporiatic; antiasthmatic; cardiant; antiparastic; antibacterial; immunosuppressive; Crohn's disease; multiple sclerosis; rheumatoid arthritis. neutralising antibody; interleukin-12; mentarity determining region; CDR; anti antiinflammatory;

Anti-hIL12

antibody H chain V region amino

acid sequence

SEQ

ij

666.

28-SEP-2000. WO200056772-A1.

24-MAR-2000; 2000WO-US07946.

25-MAR-1999; 99US-0126603

(BADI ) BASF AG.
GENETICS INST INC.

Kaymakcalan Veldman GM, Derbyshire E Salfeld JG, Roguska M, Labkovsky s, Paskind M, Paskind M, Banerjee S, Tracey DE, White M;
B, Sakorafas P, Friedrich S, Myles A;
Warne NW, Widom A, Elvin JG, Duncan AR;
Smith S, Holtet TL, Du Fou SL;

WPI; 2000-638250/61.

New human antibody specific for human interleukin-12 (IL-12) used to treat disorders characterized by aberrant IL-12 expression e.g. Crohdisease and multiple sclerosis -

```
Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardioval
 cardiovascular
```

RESULT 8
ABG91901
ID ABG
XX ABG
XX ABG
XX Hum
XX Hum
XX Hum
XX Hum
XX Fes
XX 100
XX 10 This invention relates to a new human antibody specific for human continues interleukin-12 (IL-12). The invention also includes antigen binding portions that bind to IL-12. Sequences AAB39485-B39516 represent human continues that bind to IL-12. Sequences AAB39485-B39516 represent human continues that bind to IL-12. Sequences AAB39485-B39516 represent human continues are sequences. Other variable region and no acid sequences are given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39772-B40063 represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063 represent other CDR sequences. Light chain CDR3 consensus sequences are given in AAB40064-B40067. Primers used in the identification and construction of the antibodies of the invention are given in AAG61062-C61071. The antibody of the invention is a neutralising C AAC61062-C61071. The antibody of the invention is a neutralising cantibody and has antirheumatic; antisportatic; antischerotic; cardiant; antiparasitic; antibacterial and immunosuppressive activity. The antibodies or antigen-binding fragments are useful in the treatment confidence or antigen-binding fragments are useful in the treatment. Matches Query Match Best Local : Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet function; sulphated tyrosine-dependent protein-protein interaction. Human antibody fragment #85. ABG91901 standard; 04-DEC-2002 of disorders associated with detrimental release of human IL-12 especially Crohn's disease, multiple sclerosis and rheumatoid a They can also be used in the manufacture of a pharmaceutical co Claim Lazarovits Szanthon E, 29-DEC-2000; 2000US-258948P. 29-DEC-2000; 2000US-0751181. 31-DEC-2001; 2001WO-US49442 WO200253700-A2 (BIOT-) BIO-TECHNOLOGY GEN CORP 11-JUL-2002 æ treat human IL-12 disorders. 2002-674776/72. 75; 50 NIKODGSEKYYVDSVKG 1 NIKODGSEKYYADSVRG 17 15; Similarity Page 122; 377pp; English ٦ 98 , Hagai Richter Conservative (first entry) AA, Protein; 98 92.1%; Ήĸ Plaksin Amit B, 66 <u>ب</u> Score 82; DB Pred. No. 3.4e 1; Mismatches B D, Vogel T,
Kooperman L, 3.4e-06; DB 21; Nimrod A, Length 98, Indels Mar-Haim Levanon 0 composition ÞΉ 0

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important in physiological phenomena such as cell rolling, metastasis and inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune disease, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-matrix, platelet-matrix, cell-matrix, platelet-matrix, platelet-matrix,
Sequence
 Disclosure; Page 268; 310pp; English
 protein-protein interactions. This sequence represents a human antibody
 of the invention.
98
Ã,
 relates to an isolated epitope present on cancer cells and physiological phenomena such as cell rolling, metastasis and
```

문 Ś Matches Query Match Best Local 50 NIKODGSEKYYVDSVKG 15; Н Similarity NIKQDGSEKYYADSVRG 17 Conservative 92.1%; 88.2%; 66 ۲. Score 82; DB 23; Pred. No. 3.4e-06; Mismatches Length 98 Indels ٥, Gaps

0

RESULT 9
ABG70LT
ABG70LT
ABG70
ABG70
ABG70
AC ABG7
AC Human Fv molecule hypervariable region related peptide #85 ABG78210 standard; Protein; 15-NOV-2002 ABG78210; (first entry) 98 B

Human; Fv disulfide disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma; lymphoma; myeloma; blastoma; seminoma; melanoma; acute myeloid leukaemia. molecule; hypervariable region; single chain Fv; cytostatic; Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adeno

Homo sapiens.

WO200259264-A2.

01-AUG-2002.

31-DEC-2001; 2001WO-US49440

29-DEC-2000; 2000US-0751181.

(BIOT-) BIO-TECHNOLOGY GEN CORP.

Hagai Y, Plaksin D 'n Lazarovits D, Peretz T; ŗ Guy R, Lipschitz O, Szanton 'n Levanon

WPI; 2002-619166/66.

Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of other favour of other

Claim 13; Page 191-192; 232pp; English

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```
RESULT 10
AAR66301
ID AAR66301
XX AAR66
AC AAR66
AC AAR66
XX DT 25-MA
DT 02-MU
XX COSMI
XX Prime
KW COSMI
XX Homo
ON WO942
XX 10-MJ
XX 10-MJ
XX 10-MJ
XX PT DNA
PT CC
CC Prot
CC CAmpll
CC CAmpll
CC CAmpl
 The invention relates to a peptide or polypeptide comprising an Fv CC molecule, a construct or fragments or a construct of a fragment with CC enhanced binding characteristics which selectively and/or specifically CC binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in CC association with or attached, coupled, combined, linked or fused to a continuous control of the medicament has activity against a diseased cell, preferably a cancer CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, CC myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an CC composition for use in inhibiting the growth of a diseased or cancer CC cell. This sequence represents a human Fv molecule hypervariable region CC related peptide of the invention.
 Query Match
Best Local
 Matches
protein sequences (AAR66295-51) are novel human immunoglobulin heavy chain sequences encoded by novel isolated genes. The genes (AAQ78939-79002) were isolated and cloned from a series of cosmid constructs; Y202; Y103; Y21; Y6;Y24; 3-31; M84; M118 and M.31, by PCF amplification using primers AAQ78917-38. The genes are subdivided in families of Vh genes. The fragments cover a region of 800 kb. The fragments were isolated from high molecular weight DNA from human placenta. The DNA was partially digested with TagI restriction enzyment fragments were separated by gel elecrophoresis and 35-45 kb fract
 Sequence
 25-MAR-2003
02-AUG-1995
 Claim 17; Page 40-41; 130pp; Japanese.
 DNA fragment comprising human immunoglobulin Vh
 10-MAY-1993;
 WO9426895-A1
 Homo sapiens
 cosmid;
 Human
 AAR66301 standard;
 (NISB)
 10-MAY-1993;
 1995-006791/01.
 'n
 immunoglobulin variable
 50
 1 NIKODGSEKYYADSVRG
 l Similarity
 JAPAN
 placenta;
 NIKQDGSEKYYVDSVKG
 Matsuda F;
 98
 Conservative
 amplify;
 (updated)
(first entry)
 A,
 TOBACCO
 93WO-JP00603
 93WO-JP00603
 vector;
 Protein; 117
 92.1%;
 human;
 pJB81; E.coli; mammalian.
 17
 66
 Score 82; DB
Pred. No. 3.4e
1; Mismatches
 immunoglobulin; variable; heavy
 heavy chain
 B
 ; DB 23;

3.4e-06;

1;
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 Length 98;
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RESULT 12 AAO14049

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RESULT 11
AAB62776
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 vector pJB81. The linto E.coli 490A. The hybridisation. The waseful in producing by
 The present invention provides the protein and coding sequences for the variable regions of human monoclonal antibodies which are immunoreactive with human immunodeficiency virus-1 (HIV-1) envelope glycoprotein gp120. These can be used in diagnosis and therapy of HIV-1 infection.
 03-APR-2001
 Sequence
 Novel human monoclonal antibody immunoreactive with human immunodeficiency virus-1 glycoprotein gp120, useful for detecting HIV-1 in biological sample and providing passive immunotherapy to HIV-1
 Watkins BA,
 30-JUN-1999;
 04-JAN-2001.
 Homo sapiens
 envelope glycoprotein;
 Human immunodeficiency virus-1; HIV-1; human monoclonal antibody;
 Human
 AAB62776;
 AAB62776
 were collected.
 Sequence
 Claim 1; Page 69-70;
 infected mammal
 WPI; 2001-112438/12.
 23-JUN-2000; 2000WO-US17327
 WO200100678-A1
 (USSH) US
 Local
 HIV-1 monoclonal
51
 69
 1 NIKQDGSEKYYADSVRG
 15;
 l Similarity
15; Conserv
 AAF29077
 Similarity
 NIKQDGSEKYYVDSVKG
 NIKQDGSEKYYADSVRG
 standard;
 NIKODGSEKYYVDSVKG
 g
 125
 DEPT HEALTH & HUMAN
 117
 ted. The fragments were ligated with ClaI-digested cosmic 1. The ligation products were in vitro packed and infecte 490A. The fragments were then subcloned by colony on. The Vh genes and the DNA fragments encoding them are roducing human immunoglobulin in mammalian hosts.

25-MAR-2003 to correct PN field.)
 Conservative
 Conservative
 Reitz MS
 (first
 99US-0141701.
 Ā
 A
 Protein;
 92.1%;
 entry)
 92.1%;
88.2%;
 81pp; English
 gp120; diagnosis
 antibody
 85
 17
 67
 17
 Score
Pred.
 Score 82; DB 22;
Pred. No. 4.5e-06;
 SERVICES.
 SEQ
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 Mismatches
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 4.2e-06;
 DB 16;
 Length 117;
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ABP45878
ID ABP45
XX ABP45
XX ABP45
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XX ABP45
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 Query Match
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Matches 15
 The present invention relates to a human or humanised antibody (Ab) which specifically binds to fibroblast activating protein alpha (FAPalpha). The antibodies are useful for preparing a composition for the treatment of cancer, and for imaging tumours associated with activated stromal fibroblasts, such as colorectal cancer, non-small-cell lung cancer, breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
 Park J,
Schmidt
 New human humanized antibody that specifically binds to fibroblasts activating protein alpha, useful for treating cancer or tumor, and for imaging tumors associated with activated stromal fibroblasts, e.g. lung
 BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 Sequence
 cancer, pancreatic cancer and metastatic brain cancer, and diseases associated with the same, such as inflammation and wound healing. The present sequence is a polypeptide described in the exemplification of
 ç
 Homo sapiens.
 Human anti-FAPalpha antibody
 ABP45878
 ABP45878 standard; Protein; 241
 Claim 16;
 N-PSDB;
 17-MAR-2000;
11-SEP-2000;
 WO200168708-A2
 08-AUG-2002
 AA014049
 19-AUG-2002
 16-MAR-2001; 2001WO-EP04716
 20-SEP-2001
 (BOEH)
 breast cancer
 invention.
 therapy;
 2002-041180/05
 BLyS
 50
 1 NIKODGSEKYYADSVRG
 15;
 FAPalpha;
 Similarity
 AAK98398
 A;
 BOEHRINGER INGELHEIM PHARMA KG
 Garin-Chesa
 standard;
 Page
 134
 binding
 Conservative
 2000DE-1013286.
2000GB-0022216.
 (first
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 cancer;
 B
 43; 109pp;
 fibroblast
cer; wound
 BCFV
 Protein;
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 92.1%;
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 English
 66
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 activating protein alpha; antibody; healing; inflammation; cytostatic.
 Score 82; DB 23;
Pred. No. 4.9e-06;
 fragment VH50
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 Mismatches
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Matches 15
immunosuppressive; immunostim
antiAIDS; vaccine; cancer; im
systemic lupus erythematosus;
 BLys; B lymphocyte stimulator;
tumour necrosis factor; B cell
 and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression administered to treat diseases associated with aberrant BLyS expression
 This invention describes novel antibodies that immunospecifically B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of tumour necrosis factor (TWF) super family and induces B cell proliferation and differentiation. The antibodies of the invention
 Antibodies against the diagnosis and t
 systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 Human
 Sequence
 WPI; 2002-114799/15
 Ruben
 16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240816P.
 ABP45459;
 ABP45459 standard;
 acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
the antibodies and fragments of the antibodies described in the method
 Claim
 25-MAY-2001;
 21-MAR-2001;
 10-JAN-2002
 Homo sapiens.
 19-AUG-2002
 15-JUN-2001;
 (CAMB-)
 (HUMA-)
 L6-MAR-2001;
 the invention.
 SM,
 BLyS binding scrv
 50
 1; Page 2655-2656; 3148pp; English
 15;
 Similarity
 CAMBRIDGE
 HUMAN
 NIKODGSEKYYADSVRG
 NIKQDGSEKYYVDSVKG
 Barash
 241 AA;
 2000US-240816P.
2001US-276248P.
2001US-277379P.
2001US-293499P.
 Conservative
 2001WO-US19110
 (first
 ainst B Lymphocyte Stimulating and treatment of cancers and
 GENOME SCI IN IDGE ANTIBODY
 SC,
 stimulator; TNF superfamily; human; cytostatic; ctor; B cell proliferation; B cell differentiation; immunnostimulant; immunnodulatory; antirheumatic; cancer; immune; autoimmune disorder; immunodeficies
 Protein;
 entry)
 92.1%;
 SCI INC
 Choi GH,
 SEQ
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 66
 TECHNOLOGY.
 247
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 Score 82;
Pred. No.
 1470
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immune disorders
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 Length 241;
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CVID;

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RESULT 15
ABP45583
ID ABP45
XX ABP45
XX 19-AU
DT 19-AU
XX BLys;
KW tumou
KW immun
KW antiA
KW syste
KW commo
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 Query Match
Best Local
 Matches
 B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. The also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and activity may also be
BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method
 16-JUN-2000; 2000US-212210P.
17-OCT-2000; 2000US-240B18P.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
 Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders -
 Human BLyS binding
 19-AUG-2002
 ABP45583;
 ABP45583 standard; Protein; 251
 Sequence
 This invention describes novel
 Claim 1;
 WPI;
 Ruben
 15-JUN-2001; 2001WO-US19110.
 10-JAN-2002
 WO200202641-A1
 Homo sapiens
 common variable
 (HUMA-)
 2002-114799/15
 NS.
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 invention.
 HUMAN GENOME SCI INC.
CAMBRIDGE ANTIBODY TECHNOLOGY.
 Similarity
 NIKQDGSEKYYVDSVKG
 NIKODGSEKYYADSVRG
 Page 2157-2158; 3148pp; English.
 247
 Barash SC,
 Conservative
 (first entry)
 Š
 immunodeficiency; acquired immunodeficiency syndrome.
 scFv SEQ ID 1594.
 92.1%;
 Choi GH,
 66
 17
 Score 82; DB 23;
Pred. No. 9.8e-06;
1; Mismatches 1;
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Search completed: January 12, 2004, 06:58:52 Job time : 41.1719 secs

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 Matches
 This invention describes novel antibodies that immunospecifically bind B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLys and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases.
 Sequence
 diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
 Claim 1; Page 2305-2306; 3148pp; English
 Antibodies against B Lymphocyte Stimulating the diagnosis and treatment of cancers and i
 Homo sapiens.
 of the invention.
 Ruben
 17-OCT-2000;
16-MAR-2001;
 15-JUN-2001; 2001WO-US19110
 WO200202641-A1
 25-MAY-2001;
 16-JUN-2000; 2000US-212210P.
 10-JAN-2002
 (CAMB-)
 (HUMA-)
 2002-114799/15.
 SM,
 50
 1 NIKODGSEKYYADSVRG
 l Similarity
 HUMAN GENOME
CAMBRIDGE ANT
 NIKODGSEKYYVDSVKG
 Barash SC,
 251 AA;
 Conservative
 2001US-277379P.
2001US-293499P.
 2000US-240816P.
2001US-276248P.
 ANTIBODY TECHNOLOGY.
 92.1%;
 Choi GH,
 17
 99
 Score
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 Mismatches
 82;
No.
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 polypeptides, u immune disorders
 Hilbert
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 Length 251;
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BLyS

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Result
No.
 Post-processing: Minimum Match 0% Maximum Match 10
 Minimum DB
Maximum DB
 Database :
 Total number of hits satisfying chosen parameters:
 Scoring table:
 Perfect score:
 Title:
 8
 protein -
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 US-09-829-495-63
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 Gapop 10.0 , Gapext 0
 Listing first 45 summaries
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/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
 멺
 100%
 US-09-070-356-6

US-08-113-890-2

US-09-328-352-7181

US-07-942-245-36

US-07-942-245-36

US-07-942-245-36

US-07-942-245-38

US-07-942-31673

US-09-252-991A-31673

US-08-555-386-11

US-08-452-083-2

US-08-452-083-2

US-08-452-028-2

US-08-822-028-2

US-08-822-028-6

US-08-822-028-6

US-08-822-028-6

US-08-822-028-6

US-08-822-028-30

US-08-822-028-30

US-08-822-028-30

US-08-823-028-30

US-08-951-309-48
 US-09-832-312-63
US-09-055-097-5
US-08-488-961-4
US-08-973-297-4
PCT-US96-06511-4
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 SUMMARIES
Sequence 63, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 7181, Appli
Sequence 36, Appli
Sequence 36, Appli
Sequence 38, Appli
Sequence 31673, A
Sequence 11, Appli
Sequence 2, Appli
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Sequence 2, Appli
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Sequence 30, Appli
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 Patent No.
Sequence 1
 Description
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		46.2	46.2	46.2	46.2	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	
		623	363	363	363	7257	7257	7257	7257	7257	7257	7257	495	288	288	271	271	150	134	
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		Sequence 2, Appli	Sequence 7, Appli	Sequence 7, Appli	•	•	-	•	•	•	Sequence 5, Appli	Sequence 5, Appli	Sequence 20739, A	Sequence 2, Appli	Sequence 2, Appli		Sequence 4, Appli	Sequence 2, Appli	Sequence 49, Appl	

#### Sequence 63, Application US/09832312 Patent No. 6548741 GENERAL INFORMATION: APPLICANT: Busfield et al. TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF FILE REFERENCE: 7853-234 CURRENT APPLICATION NUMBER: US/09/832,312 CURRENT FILING DATE: 2001-04-09 PRIOR APPLICATION NUMBER: 09/610,118 PRIOR APPLICATION NUMBER: 09/610,387 PRIOR FILING DATE: 2000-06-30 PRIOR FILING DATE: 2000-06-30 PRIOR APPLICATION NUMBER: 09/454,824 PRIOR FILING DATE: 1999-12-06 PRIOR FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 78 COPTEMBRE OF SEG ID NOS: 78 Sequence 5, Application US/09055097 Patent No. 5955282 GENERAL INFORMATION: APPLICANT: Hillman, Jennifer L. APPLICANT: Guegler, Karl J. APPLICANT: Corley, Neil C. APPLICANT: Shah, Purvi 밁 US-09-832-312-63 US-09-055-097-5 RESULT 2 US-09-832-312-63 SOFTWARE: FastSEQ for Windows Version SEQ ID NO 63 Query Match Best Local Similarity Matches LENGTH: 14 TYPE: PRT ORGANISM: Homo sapiens CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Ph APPLICANT: Patterson, Chandra TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR NUMBER OF SEQUENCES: 7 14; 1 DKWEAYITPGAFDV 14 DKWEAYITPGAFDV 14 3: Incyte Pharmaceuticals, 3174 Porter Drive Conservative 100.0%; Chandra 0; Score 80; I Pred. No. 7. Mismatches DB 4; ; ; 7.7e-07; Length 14; Indels .. Gaps

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STREET:

COUNTRY:

USA

Palo Alto California

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 US-08-488-961-4
 CLONE:
US-09-055-097-5
 Sequence 4, Applic
Patent No. 5606042
 Matches
 Query Match
 COMPUTER READABLE FORM:
MEDIUM TYPE: PLODBY disk
COMPUTER: IBM PC compartible
COMPUTER: PBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,961
 GENERAL INFORMATION:
 TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO:
 TYPE: emino acid
STRANDENESS: sinc
STRANDENESS: sinc
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1150971
 NAME: Cerrone, Michael C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PR-
TELECOMMUNICATION INFORMATION:
 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Reising, Ethington, Barnard & Perry
STREET: P.O. Box 4390
 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
 PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
 APPLICANT: Smith, Daniel of APPLICANT: Walker, John C
 NUMBER OF SEQUENCES:
 ITLE OF INVENTION:
 APPLICATION NUMBER: US/09/0: FILING DATE: Filed Herewith CLASSIFICATION:
 Local
 APPLICATION NUMBER: FILING DATE:
 COMPUTER: IBM Compatible
 COUNTRY: US ZIP: 48099-4390
 TELEPHONE:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-320 (UMO)
 FILING DATE:
 ENGTH:
 229 DRWPPYVTAGAF 240
 1 DKWEAYITPGAF 12
 n 58.8%;
Similarity 58.3%;
7; Conservative
 Application US/08488961
 Michigan
 325 amino acide
 Smith, Daniel S.
 (650) 855-0555
 Diskette
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 Glycine and Phaseolus alpha-D-Galactosidases
 US/09/055,097
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 PF-0490 US
 Score 47;
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 Mismatches
 Version
 DB 2;
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 Length 325
 Indels
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RESULT 5 PCT-US96-06511-4

Sequence 4, Application PC/TUS9606511

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RESULT 4
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 US-08-973-297-4
 US-08-488-961-4
 Patent No. 618401
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 TELEFAX: (810) 539-505
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 APPLIANCE APPLIANCE APPLIANCE APPLIANCE APPLIANCE: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AG
 GENERAL INFORMATION:
 APPLICANT:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 09
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 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 NUMBER OF SEQUENCES:
 51.2%;
Local Similarity 46.2%;
tes 6; Conservativo
 / Match 51.2%;
Local Similarity 46.2%;
nes 6; Conservative
 TOPOLOGY: linear
88-961-4
 STRANDEDNESS:
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 TELEPHONE:
 ENGTH:
201 DKWASYAGPGGWN 213
 201 DKWASYAGPGGWN 213
 1 DKWEAYITPGAFD 13
 1 DKWEAYITPGAFD 13
 48334
 H: 363 amino acids amino acid
 Farmington Hills
 Application US/08973297
 Michigan
 E: Kohn & Associates
30500 No. 6184017thwestern Hwy., Suite 410
 Walker, John C.
 (810) 689-4071
 Smith, Daniel S.
 (010)
 (810) 689-3500
 single
 539-5050
539-5055
 Glycine and Phaseolus alpha-D-Galactosidases
 30,955
 4.
 4.
 Score 41;
Pred. No.
 Score 41;
Pred. No.
 Mismatches
 Version
 DB 3;
 DB 1;
 Length 363;
 Length 363
 Indels
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 Gaps
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 RESULT 6
 US-09-070-356-6
 °CT-US96-06511-4
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GENERAL INFORMATION:
 GENERAL INFORMATION:
APPLICANT: Smith, Daniel S.
APPLICANT: Walker, John C.
TITLE OF INVENTION: Glycine and Phaseolus
TITLE OF INVENTION: alpha-D-Galactosidases
NUMBER OF SEQUENCES: 11
 TITLE OF INVENTION: Enz
TITLE OF INVENTION: Sai
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-505
TELEPAX: (810) 539-505
INFORMATION FOR SEQ ID NO: 4:
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (ASCII)
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APPLICATION NUMBER: US/09/070,356
 SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
STRANDEDNESS: single
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,9
REFERENCE/DOCKET NUMBER:
 TITLE OF INVENTION:
 APPLICANT: Alex Zhu
APPLICANT: Jack Goldstein
 CORRESPONDENCE ADDRESS:
 CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10016
 STREET: 30500 Northwest CITY: Farmington Hills
 APPLICATION NUMBER: PCT/US96/06511 FILING DATE:
 COUNTRY:
 STREET:
 ADDRESSEE:
 TOPOLOGY:
 CLASSIFICATION:
 ADDRESSEE:
 201 DKWASYAGPGGWN 213
 1 DKWEAYITPGAFD 13
 48334
 Application US/09070356
 Michigan
 E: Amster, Roti
90 Park Avenue
 30500 Northwestern Hwy., Suite 410
 Conservative
 linear
 Kohn & Associates
 51.2%;
 Said Enzyme
 Acetylgalactosaminidase Enzyme and cDNA Encoding
 Recombinant a-N-
 Rothstein & Ebenstein
 30,955
 0994.00050
 Score 41;
Pred. No.
 Mismatches
 DB 5;
 Length 363;
 Indels
 0
 0
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 ; RELEVANT RESIDUES IN SEQ ID NO: US-09-070-356-6
 TITLE: Cloni
Patent No. 6228631
 Matches
 Query Match
Best Local Similarity
 TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 ORGANELLE: 1ib
IMMEDIATE SOURCE: 1ib
POSITION IN GENOME: u
CHROMOSOME/SEGMENT:
MAP POSITION:
 FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: guar plant Cyamopsis tetragonoloba
 DESCRIPTION: OHYPOTHETICAL: no ANTI-SENSE: Yes
 NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: 63475/12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-5995
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/0.
FILING DATE: March 26, 1.
ATTORNEY/AGENT INFORMATION:
 PUBLICATION INFORMATION:
 MOLECULE TYPE:
 TITLE: the a-Galactosidase cDNA From TITLE: Cyamopsis tetragonoloba (guar)
 UNITS:
 CELL TYPE:
 DEVELOPMENTAL STAGE: HAPLOTYPE:
 TYPE: amino acid
STRANDEDNESS: dou
 FILING DATE:
PUBLICATION DATE:
 DATE: 1989
 PAGES:
 JOURNAL: PI
 OTHER INFORMATION:
 CLASSIFICATION:
 DOCUMENT NUMBER:
 AUTHORS:
 IDENTIFICATION METHOD:
 NAME/KEY:
 TISSUE TYPE:
 INDIVIDUAL ISOLATE:
 IOPOLOGY:
 ENGTH:
248 DKWASYAGPGGWN 260
 1 DKWEAYITPGAFD 13
 6
 541-550
 : Overbeeke et al
Cloning and Nucleotide Sequence
 411
 Conservative
 Plant Molecular Biology
 guar a-galactosidase
 linear
 cDNA to mRNA
 double
 unknown
 51.2%;
 08/037,248
 Score 41;
Pred. No.
 Mismatches
 ; DB 3;
 Length 411;
 Indels
 <u>.</u>.
 Gaps
```

RESULT 7
US-08-113-890-2
i Sequence 2, Application US/08113890
Patent No. 6329191
GENERAL INFORMATION:

IVY, JOHN M

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밁
 S
 8
 ঠ
 US-08-113-890-2
 Query Match
Best Local Similarity 40...
Conservative
 GENERAL INFORMATION:
APPLICANT: GAIY L. Breton et al.
APPLICANT: GAIY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7181
LENGTH: 810
TYPE: PRT
 Sequence 7181, Ap
Patent No. 656295
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,890
FILING DATE: 30-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
 Query Match
 ORGANISM: Acinetobacter baumannii -09-328-352-7181
 INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acids
 NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4733-0002.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
 TITLE OF INVENTION: RECOMBINANT COFFEE BEAN TITLE OF INVENTION: ALPHA-GALACTOSIDASE NUMBER OF SEQUENCES: 2
 TOPOLOGY: linear MOLECULE TYPE: protein
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER STREET: 2000 Pennsylvania Ave. N.W. CITY: Washington, D.C.
 TYPE: amino acid TOPOLOGY: linear
 TELEPHONE: (202) U. TELEPHONE: (202) 887-0763
 Local Similarity 77.8
 COUNTRY:
160
 258 DKWASYAGPGGWN 270
 5 AYITPGAFD 13
 20006-1812
SYATPGAFD 168
 DKWEAYITPGAFD 13
 90-4030
 USA
 Application US/09328352
 CLEMENTS,
 51.2%;
 46.2%;
 DAVID E.
 Mismatches
 Score 41; DB of Pred. No. 95; 1; Mismatches
 Score 41; DB
Pred. No. 49;
 4
 Length 810;
 Length 420;
 Indels
 0
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RESULT 9

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US-07-942-245-32
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 ; MOLECULE TYPE: peptide US-07-942-245-32
 US-07-942-245-36
 RESULT 10
 Sequence 36, Apr-
 Sequence 32,
Patent No. 5
 Query Match
Best Local (
 Matches
 TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
SEQUENCE 117 amino acids
 APPLICATE: 09-SEF-10-1
FILING DATE: 09-SEF-10-1
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TOTOPHONE: (202) 293-7060
 GENERAL INFORMATION: APPLICANT: PEDERS
 ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 APPLICANT: GUILD,
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
 APPLICANT:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES: 5
 APPLICANT:
 NUMBER OF SEQUENCES:
 STREET: 2100
 TITLE OF INVENTION:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
SOFTWARE: In house
 STREET: 2100 Pens
CITY: Washington
 TYPE: amino acid TOPOLOGY: linear
 COUNTRY:
 COUNTRY: United ZIP: 20037-3202
 ADDRESSEE:
 ADDRESSEE:
 INFORMATION:
 46 EWVAYISSGSFTI 58
 50.0%;
Similarity 46.2%;
6; Conservation
 2 KWEAYITPGAFDV 14
 D.C.
 Application US/07942245
 Application US/07942245
 E: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pensylvania Avenue, N.W.
 E: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pensylvania Avenue, N.W.
 United States
 United States
 SEARLE,
 ROGUSKA,
 SEARLE,
 ROGUSKA,
 REES,
 PEDERSEN,
 PEDERSEN, Jan T
 Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
 ANTIBODIES
 Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
 522
 Stephen M.J
 Michael
 Anthony
 Stephen
 32:
 Score 40;
Pred. No.
 Mismatches
 DB 1;
 Length 117;
 Indels
 0
 Gaps
```

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 US-07-942-245-38
 RESULT 11
 US-07-942-245-36
 US-07-942-245-38
 Matches
 Query Match
Best Local (
 Matches
 Query Match
Best Local
 Patent No.
 TELEX: 6491103
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
 APPLICATE: 09-SEF-12-
FILING DATE: 09-SEF-12-
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TOTO TO THE TOTO THE TOTO TO THE TOTO THE
 GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9000/700 Workstation
OPERATING SYSTEM: UNIX
 TOPOLOGY: linear MOLECULE TYPE: peptide
 CURRENT APPLICATION DATA:
 MOLECULE TYPE: peptide
 SOFTWARE: In house CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 TITLE OF INVENTION:
 APPLICANT:
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 APPLICANT:
 TYPE: amino acid
TOPOLOGY: linear
 TOPOLOGY:
 APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
 COUNTRY:
 CLASSIFICATION:
 APPLICATION NUMBER:
 SOFTWARE:
 ADDRESSEE:
 LENGTH:
 46 EWVAYISSGSFTI 58
 2 KWEAYITPGAFDV 14
 Similarity
 20037-3202
 Similarity 6; Conserv
 Washington
 6.
 amino acid
KWEAYITPGAFDV 14
 D.C.
 6491103
 Application US/07942245
 E: Sughrue, Mion, Zinn, Macpeak & Seas
2100 Pensylvania Avenue, N.W.
 117 amino acids
 REES,
ROGUSKA,
 SEARLE,
 United States
 GUILD,
 Conservative
 In house
 Conservative
 09-SEP-1992
 50.0%;
 Anthony R.
Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
 50.0%;
 Jan
 Stephen M.J
 US/07/942,245
 36:
 4; Mismatches
 Score 40;
Pred. No.
 4.
 Score 40; DB 1;
Pred. No. 20;
 Mismatches
 DB 20;
 Length 117;
 Length 117;
 Indels
 Indels
 0
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 Gaps
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 밁
 S
 RESULT 12
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 Matches
 Query Match
Best Local S
 Matches
 Query Match
 APPLICANT:
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밁
 ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31673
 PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31673
LENGTH: 546
 US-09-252-991A-25177
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US-08-565-386-11
 RESULT 13
US-09-252-991A-31673
 US-09-252-991A-25177
 SEQ ID NO 25177
LENGTH: 310
TYPE: PRT
 Sequence 11, Application US/08565386 Patent No. 5741697
 GENERAL INFORMATION:
APPLICANT: Marc J.
 Sequence 25177, Ap
Patent No. 6551795
 Sequence 31673, Application US/09252991A Patent No. 6551795
 GENERAL INFORMATION:
 TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107
 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-
 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
 TITLE OF INVENTION:
 GENERAL INFORMATION:
 CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18
 NUMBER OF SEQ ID NOS:
 FILE REFERENCE:
 ORGANISM: Pseudomonas aeruginosa
 TITLE OF INVENTION:
 APPLICANT:
 Local Similarity nes 7; Conserv
 275 DAWSASSWPGAFE 287
 529 DRFGAYDKPGAVDI 542
 46 EWVAYISSGSFTI 58
 1 DKWEAYITPGAFD 13
 1 DKWEAYITPGAFDV 14
 Similarity 7; Conserv
 Conservative
 Conservative
 Bavoil, Patrik
Hsia, Ru-ching
 Application US/09252991A
 ON: AERUGINOSA FOR DIAGNOSTICS
 107196.136
 UMBER: US 60/094,190
1998-07-27
 UMBER: US 60/074,788
1998-02-18
 Rubenfield et al.
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
 1998-02-18
 AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 48.8%;
53.8%;
 Patrik M.
 48.8%;
BACTERIOPHAGE OF CHLAMYDIA PSITTACI
 US 60/074,788
 Score 39;
Pred. No.
 Score 39;
Pred. No.
 Mismatches
 Mismatches
 DB 4;
1.3e+02;
 76;
 DB 4;
 Length 546;
 Length 310;
 ٥.
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 Gaps
 PSEUDOMONAS
 0
 0
```

NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:

ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP STREET: Clinton Square, P.O. Box 1051

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밁
 Ś
 RESULT 15
US-08-452-083-2
 Best Loc
Matches
 CURRENT APPLICATION NUMBER: US/08/952,
APPLICATION NUMBER: US/08/952,
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/305, 765
FILING DATE: 13-SEP-1994
ATTORNEY/ACENT INFORMATION:
NAME: Brook, David E.
NAME: Brook, David E.
 Sequence 2, Application US/08452083
Patent No. 5756327
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Sassanfar, Mandana
APPLICANT: Schimmel, Paul R.
TITLE OF INVENTION: RECOMBINANT MYCOBACTERIAL ISOLEUCYL-tRNA
TITLE OF INVENTION: SYNTHETASE GENES, TESTER STRAINS AND ASSAYS
 COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENTIN Release #1.0, Ver

CURRENT APPLICATION DATA:

**POT TOATTON NUMBER: US_08/452,083
 Query Match
 MOLECULE TYPE: peptide -08-565-386-11
 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 176/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 716-263-1636
 TELEFAX: 716-263-1600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP
TELECOMMUNICATION INFORMATION:
 NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook,
STREET: Two Militia Drive
 STREET: C. STREET: C. Roches
 Local
 STRANDEDNESS:
TOPOLOGY: 1i
 APPLICATION NUMBER: FILING DATE:
 STREET: Two Mil.
 TYPE: amino acid
 COUNTRY:
 ENGTH:
 94 DNWESFITGG 103
 1 DKWEAYITPG 10
 Similarity 60.
 Massachusetts
 USA
 linear
 not relevant
 48.8%;
 US/08/565,386
 Score 39; DB 1; Length 596 Pred. No. 1.5e+02; Mismatches 2; Indels
 176/60040
 CPI94-08B
 Smith & Reynolds, P.C.
 Version #1.30
 Length 596;
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 Gaps
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0

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 ; MOLECULE TYPE: protein US-08-452-083-2
 Query Match 48.8%;
Best Local Similarity 62.5%;
Matches 5; Conservative
 TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 TYPE: amino acid
TOPOLOGY: linear
 TELEPHONE:
 ENGTH:
144 DEWOAYVT 151
 1 DKWEAYIT 8
 1045 amino acids
 (617) 861-6240
 Score 39; DB 1; Le
Pred. No. 2.6e+02;
3; Mismatches 0;
 DB 1; Length 1045;
 Indels
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0

Gaps

0

Search completed: January 12, 2004, 07:03:59 Job time: 12.5938 secs

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No.
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
 Minimum DB
Maximum DB
 Title:
Perfect score:
 Total number of hits satisfying chosen parameters:
 Scoring table:
 OM protein -
 Database
 Searched:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Score
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 protein search, using sw model
 length: 0
length: 2000000000
 Match Length
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Gapop 10.0 ,
 US-09-829-495-62
89
 328717 seqs, 42310858 residues
 1 NIKQDGSEKYYADSVRG 17
 January 12, 2004, 06:56:19;
 Query
 Issued_Patents_AA:*
 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-942-245-37
US-08-545-809A-134
US-08-545-809A-124
US-08-545-809A-124
US-08-478-039-95
US-08-478-039-95
US-08-478-039-95
US-08-478-039-95
US-08-211-202-114
US-08-211-202-114
US-08-311-398A-46
US-08-311-397B-46
US-08-311-397B-
 summaries
 SUMMARIES
 ; Search time 14.0781 Seconds (without alignments) 51.092 Million cell updates/sec
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41, Appl
41, Appl
41, Appl
42, Appl
43, Appl
44, Appl
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46, Appl
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48, Appl
49, Appl
40, Appl
41, A
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 RESULT 1
US-09-832-312-62
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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28
64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64	64
71.9	71.9	71.9				71.9		71.9	71.9	71.9	71.9	71.9				71.9	
128	128	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125	125
ب	<u>س</u>	Ŋ	ហ	ហ	ហ	v	S	μ	Н	<u>س</u> و	<b> </b> 0	<b>μ.</b>	۲	щ	<u>س</u>	سر	ш
US-08-476-349A-96	US-08-478-039-96	PCT-US95-08743-77	PCT-US95-08743-76	PCT-US95-08743-75	PCT-US95-08743-74	PCT-US95-08743-73	PCT-US95-08743-72	US-08-899-575-77	US-08-899-575-76	US-08-899-575-75	US-08-899-575-74	US-08-899-575-73	US-08-899-575-72	US-08-899-575-77	US-08-899-575-76	US-08-899-575-75	ÚS-08-899-575-74
96,	•	Sequence 77, Appl	Sequence 76, Appl	•	-	-	72,	•	-	Sequence 75, Appl	•	•	-	•	•	Sequence 75, Appl	•

#### ALIGNMENTS

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RESULT 2
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 ; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FASTSEQ for Windows Version
; SEQ ID NO 62
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-62
 FILE REFERENCE: 7853-234

CURRENT APPLICATION NUMBER: US/09/832,312

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: 09/610,118

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/503,387

PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR FILING DATE: 1999-12-06
 Sequence 37, Applicat Patent No. 5639641
GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 17; Conserv
 Sequence 62, Application US/09832312
Patent No. 6548741
 GENERAL INFORMATION
 PRIOR APPLICATION NUMBER: 09/345,468 PRIOR FILING DATE: 1999-06-30
 APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
 APPLICANT: PEDERSEN, JA
APPLICANT: SEARLE, St
APPLICANT: REES, Mi
APPLICANT: ROGUSKA, Mi
APPLICANT: GUILD, Br
TITLE OF INVENTION: SUR
TITLE OF INVENTION: ANT
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
 ADDRESSEE:
 a 37, 55.
39641
 NIKQDGSEKYYADSVRG 17
 NIKQDGSEKYYADSVRG
 Application US/07942245
 100.0%; ilarity 100.0%; Conservative (
Sughrue, Mion, Zinn, Macpeak & Seas
 EN, Jan T.
Stephen M.J.
Anthony R.
A, Michael A.
Braydon C.
SURFACE RESIDUE VENEERING OF RODENT
ANTIBODIES
SEC. 522
 17
 0
 Score 89; DB 4;
Pred. No. 4.1e-09;
Mismatches 0;
 Length 17;
 Indels
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 Gaps
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; MOLECULE TYPE: peptide US-07-942-245-37
 US-08-545-809A-95
 Sequence 95, Application US/08545809A Patent No. 6096878
 Matches
 Query Match
 GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Metsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
 TELEX: 200154
INFORMATION FOR SEQ ID NO:
 INFORMATION FOR SEQ ID NO:
 SOFTWARE: In house
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942,245
FILING DATE: 09-SEP-1992
CLASSIFICATION: 530
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
 NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 065
TELECOMMUNICATION INFORMATION:
TELECHONE: 617-542-5070
 APPLICATION NUMBER: US/08/545,809A FILING DATE: 27-MAR-1996 PRIOR APPLICATION DATA: APPLICATION UMBER: PCT/JF93/00603 FILING DATE: 10-MAY-1993 ATTORNEY/AGENT INFORMATION:
 SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HP 9007/700 Workstation
 COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
 STREET: 2100
 NUMBER OF SEQUENCES:
 TELEFAX: (202, TELEFAX: 6491103
 Local Similarity 88.1
les 15; Conservative
 TELEPHONE: (202) 293-7860
 COMPUTER: HP 9000//UV COPERATING SYSTEM: UNIX
 TELEFAX:
 TOPOLOGY:
 COUNTRY:
 STREET:
 50 NIKODGSEKYYVDSVKG 66
 1 NIKQDGSEKYYADSVRG 17
 02110-2804
 20037-320
 Boston
 ₹
 225 Franklin Street
 2100 Pensylvania Avenue, N.W.
 S
 617-542-8906
 United States
 linear
 92.1%;
 37:
 95:
 06501/004001
 Score 82;
Pred. No.
 Mismatches
 DB 1;
 2.0
 Length 98;
 Indels
 0,
 Gaps
 0
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 US-09-079-029-10
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 US-08-545-809A-95
 US-08-545-809A-134
 RESULT 5
 US-09-079-029-10
 Sequence 134, Application US/08545809A
Patent No. 6096878
 Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumil
TITLE OF INVENTION: HUMAN
 GENERAL INFORMATION:
 APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
 ATTORNEY/AGENT INFORMATION:
 SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 MOLECULE TYPE: protein
 TELECOMMUNICATION INFORMATION:
 CORRESPONDENCE ADDRESS
 TYPE: ami
 Local Similarity
 NAME: Marschang, Diane 1
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
 FILING DATE:
CLASSIFICATION:
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 CITY: South San F
STATE: California
 LENGTH:
 TOPOLOGY:
 LENGTH: 312 amino acids
TYPE: Amino Acid
 TELEPHONE:
 APPLICATION NUMBER: US/09/079,029
 COUNTRY:
 STREET:
 ADDRESSEE:
 69 NIKODGSEKYYVDSVKG 85
 15;
 89 NIKQDGSEKYYVDSVKG 105
 15;
 1 NIKODGSEKYYADSVRG 17
 1 NIKODGSEKYYADSVRG 17
 94080
 amino acid
3Y: linear
 Application US/09079029
 Adams, Camilia W.
Ashkenazi, Avi J.
 1 DNA Way
 117 amino acids
 3: 650/225-5416
650/952-9881
 USA
 Conservative
 Conservative
 Linear
 Genentech, Inc.
 Francisco
 92.1%;
 92.1%;
88.2%;
 Fumihiko
HUMAN IMMUNOGLOBULIN VH GENE
 (Genentech)
 35,600
 Score 82; DB 4;
Pred. No. 1.8e-06;
 Score 82;
Pred. No.
 P1101R2
 Mismatches
 Mismatches
 6e-07;
 DВ
 س
••
 Length 312;
 Length 117;
 Indels
 0
 0
 Gaps
 0
 0;
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 US-08-545-809A-134
 ; OTHER INFORMATION: anti-Rh(D) antibody clone SH17 US-09-240-274-141
 US-09-240-274-141
 Best Loc
Matches
 GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-42U2
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT APPLICATION NUMBER: 09/081,380
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
 Query Match
Best Local Similarity
Matches 13; Conserv
 SOFTWARE: Pa
SEQ ID NO 141
 Sequence 141, Appl
Patent No. 6255455
 Query Match
 EARLIER APPLICATION NUMBER: 60/028,550 EARLIER FILING DATE: 1996-10-11 NUMBER OF SEQ ID NOS: 224
 APPLICATION NUMBER: US/08/545
FILING DATE: 27-MAR-1996
FRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29.066
REFERENCE/DOCKET NUMBER: 0650
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
 INFORMATION FOR SEQ ID NO:
 ORGANISM: Homo sapiens FEATURE:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
 SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
 CORRESPONDENCE ADDRESS
 Local Similarity
 TOPOLOGY:
 OPERATING SYSTEM:
 CITY: Boston
 TELEFAX:
 ADDRESSEE:
 SENGTH: 116 amino acids
 68 DÍKCDGSEKYYVDSVKG 84
 1 NIKODGSEKYYADSVRG 17
 02110-2804
 PatentIn Ver.
 amino acid
GY: linear
 Application US/09240274
 225 Franklin Street
 617-542-8906
 Conservative
 SD
 Conservative
 IBM Compatible
 Fish & Richardson, P.C.
 protein
 SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
 Windows95
 75.3%;
 77.5%;
76.5%;
 US/08/545,809A
 PCT/JP93/00603
 2
 06501/004001
 Score 69; D
Pred. No. 0.
Score 67; DB 3;
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1; Mismatches 3
 Mismatches
 DB 3; Length 116;
 00011
 Length 117;
 Indels
 0;
 <u>.</u>.
 Gaps
 Gaps
 0
 0
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 Matches
 GENERAL
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 US-08-545-809A-124
 US-08-545-809A-124
 Patent No. 609687
 Patent No.
 Sequence 95, Application US/08478039 Patent No. 5681722
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 Sequence 124, Application US/08545809A
 GENERAL INFORMATION:
APPLICANT: Newman, Roland A.
APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombinant
NUMBER OF SEQUENCES: 114
 TELEX: 200154
INFORMATION FOR SEQ ID NO:
 C11.
STATE: L.
COUNTRY: US
COUNTRY: US
C0110-2804
C04DABLE F
 APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CO
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS
 NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/.
FILING DATE: 10-MAY-1993
 OPERATING SYSTEM: Windows95
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CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 225 Franklin Street
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 Local Similarity
 TOPOLOGY:
 CITY: Boston
 APPLICATION NUMBER:
CITY:
 TELEFAX:
 ADDRESSEE:
 LENGTH:
 50
 68 HIWNDGSQKYYADSVKG
 12;
 1 NIKODGSEKYYADSVRG 17
 amino acid
 NIKODGSKKNYVDSVEG
 NIKODGSEKYYADSVRG
 114 amino acids
 699 Prince St.
 617-542-8906
 Conservative
 linear
 IBM
 protein
 Compatible
 73.0%;
 PCT/JP93/00603
 US/08/545,809A
 66
 ω
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 SWECKER & MATHIS
 Score 65;
Pred. No.
 06501/004001
 Mismatches
 P.C.
 Antibodies
 0.00053;
 DB 3;
 for Human Therapy
 Length 114;
 CONTAINING THE SAME
 0;
 Gaps
 0
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COUNTRY:

USA

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 US-08-476-349A-95
 US-08-478-039-95
 Matches
 Query Match
Best Local
 Sequence 95, Application US/08476349A Patent No. 5750105
 GENERAL INFORMATION:
 TELEFAX: 703-836-2021
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: peptic
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
 ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 APPLICATION NUMBER: US 0: FILING DATE: 25-JUL-1991 ATTORNEY/AGENT INFORMATION:
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
 ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TELECOMMUNICATION INFORMATION:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 PPLICANT: Newman, Roland A.
PPLICANT: Hanna, Nabil
PPLICANT: Hanna, Nabil
PPLICANT: Raab, Ronald W.
ITLE OF INVENTION: Recombinant Antibodies for Human Therapy
UMBER OF SEQUENCES: 114
 APPLICATION NUMBER: US 08/379,072 FILING DATE: 25-JAN-1995
 FILING DATE: 0
CLASSIFICATION:
 TOPOLOGY: not relevant
 TYPE: amino acid
 REFERENCE/DOCKET NUMBER:
 APPLICATION NUMBER: US 07/912,292 FILING DATE: 10-JUL-1992
 STRANDEDNESS:
 TELEPHONE:
 NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
 FILING DATE:
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 COUNTRY:
 STREET:
 IDDRESSEE:
 ENGTH:
 MPUTER: IBM PC compatible ERATING SYSTEM: PC-DOS/MS-DOS
 51 ISDDGSNKÝÝADSVKG 66
 12;
 2 IKQDGSEKYYADSVRG 17
 Similarity
 2
 S
 699 Prince St.
 Lexandria
 126 amino acids
 USA
 Conservative
 BURNS, DOANE, SWECKER & MATHIS
 IBM PC compatible
PatentIn Release #1.0, Version #1.30
 703-836-6620
 Floppy disk
 23-MAR-1992
 07-JUN-1995
 peptide
 not relevant
 73.0%; Score 65; DB 1; Le
75.0%; Pred. No. 0.00059;
live 1; Mismatches 3;
 US 07/735,064
 US 07/856,281
 US/08/478,039
 RF SJ1
 35,030
 012712-160
 Version #1.30
 Length 126
 Indels
 <u>.</u>
 Gaps
 0
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 RESULT 10
 á
 US-08-476-349A-95
 Matches
 Query Match
Best Local :
 TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 95:
 GENERAL INFORMATION:
 ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
 SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/211,202
FILING DATB: 23-SEP-1992
CLASSIFICATION: 435
 STREET: Chicago
CITY: Chicago
TTATE: Illinois
 REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-161
TELECOMMUNICATION INFORMATION:
 MOLECULE TYPE: peptid POSITION IN GENOME: CHROMOSOME/SEGMENT:
 FILING DATE: 23-MAR-
PRIOR APPLICATION DATA:
 SEQUENCE CHARACTERISTICS
 FILING DATE: 25-JUL-1991 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 10-JUL-
PRIOR APPLICATION DATA:
 CURRENT APPLICATION DATA:
PRIOR APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 PRIOR APPLICATION DATA:
 CITLE OF
 APPLICANT:
 TELEPHONE: 703-62021
 APPLICATION NUMBER: US 07/912,292 FILING DATE: 10-JUL-1992
 NAME: Teskin Esq., Robin L
REGISTRATION NUMBER: 35,03
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 STRANDEDNESS:
 TYPE: amino acid
 APPLICATION NUMBER:
 ADDRESSEE:
 COPOLOGY: not relevant
 ENGTH:
 No
 E OF INVENTION:
 51 ISDDGSNKYYADSVKG 66
 12;
 2 IKODGSEKYYADSVRG 17
 h 73.0%; Score 65; D
Similarity 75.0%; Pred. No. 0.
 INVENTION:
 126 amino acids
 6300 Sears Tower,
 Application US/08211202
 Conservative
 BAIER, Michael
 WINTER, Gregory Paul
 HOOGENBOOM, Hendricus Renerus Jacobus Matteus
 JESPERS,
 703-836-6620
 David W. Clough, Marshall O'Toole Gerstein Murray &
 Borun
 07-JUN-1995
 peptide
 23-MAR-1992
 not relevant
 Production of chimeric antibodies - combinatorial approach
 Laurent Stephane Anne Therese
 144
 US 07/735,064
 US 07/856,281
 RF SJ1
 US/08/476,349A
 233 South Wacker Drive
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FILING DATE: 23-SEP-PRIOR APPLICATION DATA:

APPLICATION NUMBER:

GB 9120252.3

APPLICATION NUMBER:

25-SEP-1991

GB 9120377.8

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.
 RESULT 11
 ; MOLECULE TYPE: protein US-08-211-202-118
 US-08-211-202-141
 Matches
 Query Match
Best Local Similarity
 Sequence 141, Application US/08211202
 GENERAL INFORMATION:
 tent No.
 NFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IPM PC compatible
COMPUTER: COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS: LENGTH: 98 amino acids
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9120252.3
 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-474-6300
 CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
 APPLICANT:
 ATTORNEY/AGENT INFORMATION:
NAME: David W. Clough
 PRIOR APPLICATION DATA:
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 NUMBER OF SEQUENCES:
 APPLICANT:
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 TELEPHONE: 312-1,
TELEPHONE: 312-474-0448
 APPLICATION NUMBER: US/0 FILING DATE: 23-SEP-1992
 STREET:
 TOPOLOGY:
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 REGISTRATION NUMBER: 36
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 FILING DATE: 23-SEP-1991
LIOR APPLICATION DATA:
 COUNTRY:
 ADDRESSEE:
 APPLICATION NUMBER: FILING DATE: 15-MAY
 APPLICATION NUMBER:
 APPLICATION NUMBER:
 ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 51 ISYDGSNKYYADSVKG 66
 2 IKODGSEKYYADSVRG 17
 60606-6402
 Chicago
 amino acid
 Illinois
 BAIER, Michael
JESPERS, Laurent Stephane Anne Therese
WINTER, Gregory Paul
 6300 Sears Tower, 233 South Wacker Drive
 USA
 HOOGENBOOM, Hendricus Renerus Jacobus Matteus
 Conservative
 umber: PCT/GB92/00883
15-MAY-1992
 24-MAR-1992
 24-MAR-1992
 71.9%;
75.0%;
 Production of combinatorial
 144
 US/08/211,202
 GB 9206372.6
 GB 9206318.9
GB 9120377.8
 36,107
 118:
 28111/31960
 Score 64; DB 1;
Pred. No. 0.00066
 Mismatches
 chimeric antibodies - approach
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 Indels
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 Gaps
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 US-08-545-809A-115
 RESULT 12
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 Sequence 115, Application US/08545809A Patent No. 6096878
 Matches
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 INFORMATION FOR SEQ ID NO:
 INFORMATION FOR SEQ ID NO:
 FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/,
FILING DATE: 10-MAY-1993
 OPERATING SYSTEM: Wind SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
 APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
 SEQUENCE CHARACTERISTICS
LENGTH: 116 amino aci
 REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
 APPLICANT:
 FILING DATE: 25-SEP-PRIOR APPLICATION DATA:
APPLICATION NUMBER:
SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
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 CORRESPONDENCE ADDRESS:
 TELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 NUMBER OF SEQUENCES:
 TELEPHONE: 312-474-0448
 NAME: David W. Clough
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
 TELEFAX:
 STATE:
 APPLICATION NUMBER: FILING DATE: 15-MAN
 FILING DATE:
 FILING DATE:
 NAME: Freeman, John W
REGISTRATION NUMBER:
 NAME:
 APPLICATION NUMBER:
 COMPUTER:
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 COUNTRY:
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 TOPOLOGY:
 ADDRESSEE:
 INFORMATION:
 51 ISYDGSNKYYADSVKG 66
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 2 IKQDGSEKYYADSVRG 17
 02110-2804
 Boston
MA
 amino acid
 116 amino acids
 225 Franklin Street
 617-542-8906
 S
 Conservative
 Honjo,
 linear
 IBM Compatible
 Fish & Richardson, P.C.
 312-474-6300
 24-MAR-1992
 15-MAY-1992
 24-MAR-1992
 25-SEP-1991
 Tasuku
 71.9%;
 Windows95
 for Windows Version
 PCT/JP93/00603
 PCT/GB92/00883
 GB 9206372.6
 GB 9206318.9
 US/08/545,809A
 29,066
 141:
 28111/31960
 06501/004001
 Score 64; 1
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 Mismatches
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 Indels
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 Gaps
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 , MOLECULE TYPE: protein US-08-545-809A-115
 US-08-331-398A-46
 US-08-331-398A-46
 Sequence 46, Apr-
 Query Match
Best Local :
Query Match
Best Local Similarity
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 APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
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 TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
 REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
 APPLICATION NUMBER: US 0 FILING DATE: 12-OCT-1990 ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
 APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
 APPLICANT:
 APPLICANT:
 NUMBER OF SEQUENCES:
 APPLICANT:
 MOLECULE TYPE: protein
 NAME/KEY: Protein LOCATION: 1..119 OTHER INFORMATION: OTHER INFORMATION:
 Y Match 71.9%;
Local Similarity 75.0%;
les 12; Conservative
 STREET: One Market | CITY: San Francisco
 TOPOLOGY: linear
 LENGTH:
 STRANDEDNESS
TOPOLOGY: 1:
 COUNTRY:
 NAME:
 ENGTH:
 70 ISYDGSNKYYADSVKG 85
 N
 amino acida
 H: 119 amino acids
amino acid
 IKQDGSEKYYADSVRG 17
 Application US/08331398A
 Willingham, Mark
FitzGerald, David
 USA
 Brinkmann, Ulrich
 Pastan,
 linear
 ifornia
 Tom
 71.9%;
 /note= "Human fetal immunoglobulin
56P1'CL Variable Heavy chain (V-H)
 US 07/596,289
 46:
 1.
 015280-126110US
 Score 64; [
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 Score 64; DB 1;
Pred. No. 0.00082;
 Mismatches
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 .00081
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 Gaps
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 RESULT 14
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 US-08-331-397B-46
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 Sequence 46, Application US/08331397B Patent No. 5981726
 Matches
 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
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FILING DATE: 30-SEP-1991
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FILING DATE: 30-SEP-1991
PRIOR APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
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 TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
 GENERAL INFORMATION:
 ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
 TITLE OF INVENTION: TITLE OF INVENTION:
 APPLICANT:
 ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
 FEATURE:
 MOLECULE TYPE:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 NAME/KEY: Protein LOCATION: 1..119 OTHER INFORMATION: OTHER INFORMATION:
 Local
 COUNTRY:
 STATE: California
 STREET:
 NAME: Hunter, Tom REGISTRATION NUMBER:
 CITY: San Francisco
 TOPOLOGY:
 STRANDEDNESS:
 ADDRESSEE:
 ENGTH:
 51
 51 ISYDGSNKYYADSVKG
 12;
 2 IKQDGSEKYYADSVRG 17
 l Similarity
12; Conserv
 2 IKQDGSEKYYADSVRG 17
 amino acid
 ISYDGSNKYYADSVKG
 E: Townsend and Townsend and Crew
One Market Plaza, Steuart Street Plaza
 119 amino acids
 Conservative
 (415) 543-5043
 USA
 Pastan,
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 linear
 protein
 Specific Thereof
 71.9%;
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 Chimeric and Mutationally Stabilized Tumor-
Specific Antibody Fragments, Fusion Proteins, and Uses
 /note= "Human fetal immunoglobulin
56P1'CL Variable Heavy chain (V-H)"
 38,498
 66
 66
 1;
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Pred. No. 0.00
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 Mismatches
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0.00082;
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 Indels
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 Gaps
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RESULT 15 US-08-759-804A-46 ; Sequence 46, Application US/08759804A .

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 US-08-759-804A-46
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/331,398

FILING DATE: 28-OCT-1994

PRIOR APPLICATION UMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION UMBER: US 07/596,289

FILING DATE: 30-SEP-1991

PRIOR APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 015280-126140US

TREDEPANTION NUMBER: 576-0200

TELEPAN: (415) 576-0300

INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATHER:
 Query Match 71.9
Best Local Similarity 75.0
Matches 12; Conservative
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
 APPLICANT: PitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
 FEATURE:
NAME/KEY: Protein
 APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Frinkmann, Ulrich
 LOCATION: 1..119
OTHER INFORMATION:
OTHER INFORMATION:
 STATE: C.
 CITY: San Francisco
 INFORMATION:
 California
 USA
 03-DEC-1996
 71.9%; Score 64; DB 2; 75.0%; Pred. No. 0.00082;
 /note= "Human fetal immunoglobulin
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OM protein - protein search, using sw model
 Copyright
 GenCore version 5.1.6
(c) 1993 - 2004 Compugen
 Ltd
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106.117 Million cell updates/sec

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Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*

Database :

pir1:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

29	28	27	. 26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	44.	w	N	Ľ	1 20.	Result
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T17483	AH1239	AD1602	C71014	T23238	H82296	AB1989	T06388	S07472	A75328	T50781	E71624	AF0475	F87634	E90142	PH1015	C64834	H90756	F85620	E85553	B90703	C64785	T50839	T50840	T00186	S76795	T38463	H98116	B95252		<b>‡</b>
peptide synthetase	DNA polymerase III	DNA polymerase III		hypothetical prote	c-di-GMP phosphodi	hypothetical prote	alpha-galactosidas	alpha-galactosidas	PhoH-related prote	alpha-galactosidas	rifin PFB0055c - m	LysR-family transc	conserved hypothet		Ig heavy chain V r	le		partial fimbrial u		probable outer mem	outer membrane ush	U4/U6 small nuclea	U4/U6-associated R	dUTP diphosphatase	hypothetical prote		probable alcohol d	ρ,	**************************************	

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48.8	48.8	48.8 48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8	48.8
1041	766 998	592 596	495	434	367	367	366	264	179	148	115	115
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probable ileS prot DNA-directed RNA p	isp4 protein homol protein kinase AK4	phospholipase C (E	probable sulfate t	alpha-galactosidas	probable fimbrial	probable outer mem	hypothetical prote					

# ALIGNMENTS

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; on, J.D.; Umayam, L.A.; White, O.; Salzberg, Bisen, J.A.; Read, T.D.; Peterson, S.; Hei
S.L.; Lewis, M.R.; Radune, D.; Holtzapple,

S.; Heic

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, B.K.; Holt, I.E. Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A;Reference number: A95000; MUID:21357209; PMID:11463916 A; Accession: B95252

A; Molecule type: DNA A; Residues: 1-383 < KUR> A;Status: preliminary

A;Cross-references: GB:AE005672; PIDN:AAK76211.1; PID:g14973668; GSPDB:GN00164; TIGR:SP4 A;Experimental source: strain TIGR4 Genetics:

A;Gene: SP2157 C;Superfamily: lactaldehyde reductase; lactaldehyde reductase homology

Ś Best Loc Matches Query Match Local Similarity les 8; Conserv 4 EAYITPGAFDV 14 Conservative 57.5%; 72.7%; 2. Score 46; DB 2; Pred. No. 3.7; Mismatches 1: Length 383; Indels <u>.</u> Gaps

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#### RESULT 2

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199

EALVTPGAYDV 209

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C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C;Accession: H98116 **Н98116** 

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
J.; Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: H98116

A; Status: preliminary

A;Molecule type: DNA A;Residues: 1-383 <KUR> A;Cross-references: GB:AE007317; PIDN:AAL00765.1; PID:g15459663; GSPDB:GN00174

A;Gene: adh2

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C.Species: Synechocystis sp. A; Variety: PCC 6803
C; Date: 25-7-7-7
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S76795
 RESULT 3
 C; Superfamily: lactaldehyde reductase; lactaldehyde reductase homology C; Keywords: oxidoreductase; NAD
RESULT
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 R;Harris, D.; McDonald, S.; Barrell, B.G.; Rajandream, submitted to the EMBL Data Library, February 1996
 probable aminotransferase (BC 2.6.1.-) - fission yeast (Schizosaccharomyces C_iSpecies: Schizosaccharomyces pombe
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 A; Note: the nucleotide sequence
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A; Residues: 1-765 < KAN>
 A;Reference number: S74322; MUID:97061201; PMID:8905231 A;Accession: S76795
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
 A; Accession: T38463
 A; Reference number: Z21794
 ;Map position: 1
;Superfamily: beta-alanine-pyruvate transaminase
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 ;Cross-references: EMBL:Z69368; PIDN:CAA93294.1;
;Experimental source: strain 972h-; cosmid c27F1
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les 7; Conserv
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8; Conserv
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50.0%;
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 56.2%;
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 H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Mi
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da, M.; Yasud
 pombe)
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R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Biosci. Biotchem. 61, 1960-1962, 1997
A;Title: Panton-Valentine leukocidin genes in a phage-like A;Reference number: Z14119; MUID:98067870; PMID:9404084
A;Accession: T00186
 C;Species: Staphylococcus aureus phage phi PVL
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Jun-2002
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 A; Title: A new cyclophilin
A; Reference number: Z12233
 R;Horowitz, D.S.; Kobayashi, RNA 3, 1374-1387, 1997
 Hum. Mol. Genet. 6, 2117-2126, 1997
A; Title: Identification and characterization of human genes
 R; Wang, A.; Forman-Kay, J.; Luo, Hum. Mol. Genet. 6, 2117-2126, 1
 C; Superfamily: C; Keywords: hyo
 dUTP diphosphatase (EC 3.6.1.23) - Staphylococcus aureus phage phi
 A; Accession: T50839
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 A;Gene:
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A; Residues: 1-682 < WAN>
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 A; Reference number: Z12232
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 390
 108 YITPGVFDI 116
 ly: retroviral proteinase
hydrolase; nucleotide metabolism
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 6 YITPGAFDV 14
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 o, Y.; Luo, M.; Chow, Y.H.; Plumb, J.; Friesen, 1997
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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
A:Reference number: A99629; MUID:21156231; PMID:11258796
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 probable outer membrane protein ECs0594 [imported] - Escherichia coli (strain C;Species: Escherichia coli (C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
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 R; Blattner, F.R.; Plunkett I
.A.; Rose, D.J.; Mau, B.; Sh
Science 277, 1453-1462, 1997
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 A; Reference number: A99629; A; Accession: B90703
 C; Keywords: membrane protein
 outer membrane usher protein sfmD precursor - Escherichia coli (strain K-12) C;Species: Escherichia coli
E85553
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 R;Hayashi, T.;
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C;Accession: C64785
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 A;Status: preliminary
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 Superfamily: outer membrane usher protein fimD
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 Accession: B90703
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 Superfamily: outer membrane usher protein fimD
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 3 WEAYITPGAFDV 14
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protein sfmD [imported] -

Escherichia coli (strain 0157:H7, substrain

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DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
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H90756
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 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
 partial fimbrial usher protein [imported] - Escherichia coli (strain O157:H7, C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
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F85620
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 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: E85553
R;Perna, N.T.; plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, R;Perna, N.T.; portamousis.
 A;Gene: Z1289
 A; Reference number: A85480; A; Accession: F85620
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R,Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; B.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUJD:97426617; PMID:9278503
A;Accession: C64834
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 probable outer membrane usher protein ycbS - Escherichia coli (strain K-12) C_\ellSpecies: Escherichia coli
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A;Gene: ECs1024
 Ig heavy chain V region (clone 111.55) - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_C;Accession: PH1015
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 C;Accession: PH1015
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
R.Exp. Med. 176, 761-779, 1992
A;Tille: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1015
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 RESULT 13
 A;Experimental source: B cell, strain [NZB x NZW]F1 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
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A;Description: Sulfolobus solfataricus complete genome.
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E90142
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 A;Cross-references:
C;Genetics:
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A; Residues: 1-238 < KUR>
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Pred. No.
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SSRA_ARATH
PYRC_HALN1
MAC1_SCHPO
RRPO_PEAMV
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Q92396
 Q9uxd4
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Q9hmh9
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Q98028
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P22139
P233664
 Q8zaa7
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 PROSITE; PS00600; AA TRAÑSFER_CLASS_3; 1.

Hypothetical protein; Transferase; Aminotransferase;
Pyridoxal phosphate.
BINDING 305 PYRIDOXAL PHOSPHATE (DV SROHENCE 40.
 SEQUENCE FROM N.A.

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Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,

Federapiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Lin

Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;

"Sequence of minutes 4-25 of Escherichia coll.";

"Sequence of minutes 4-25 of Escherichia coll.";

"Sequence of CEC-1996) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF SFMA FIMBRIAL

SUBUNITS ACROSS THE OUTER MEMBRANE (BY SIMILARITY).
 MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
 HSSP; P12995; 1QJ3.
GeneDB_SPombe; SPAC27F1.05c; -.
InterPro; IPR005814; Aminotrans_3.
 EMBL; Z69368; CAA93294.1; PIR; T38463; T38463.
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 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
 P77438; P77133;
01-NOV-1997 (Rel. 35, Created)
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28-PEB-2003 (Rel. 41, Last annotation updat
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 SEQUENCE
Pfam; PF00577; Usher; 1. PROSITE; PS01151; FIMBRIAL_USHER; 1.
 PIR; C64785; C64785.
EcoGene; EG13883; sfmD.
InterPro; IPR000015; Fimb_usher.
 EMBL; AE000159; AAC73634.1; -.
EMBL; U82598; AAB40730.1; -.
EMBL; U82664; AAB40285.1; -.
PIR; C64785; C64785.
 Science
 Escherichia coli.
 SFMD OR B0532
 Outer membrane usher protein sfmD
 - I- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
 -!- SUBCELLULAR LOCATION: Integral
 SEQUENCE FROM N.A.
STRAIN=K12 / MG165
 NCBI_TaxID=562;
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 complete genome sequence of Escherichia coli K-12.";
nce 277:1453-1474(1997).
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 484 AA;
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 MG1655;
 STANDARD;
 53190 MW;
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 Score 46; DB Pred. No. 3; 3; Mismatches
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HAMAP; MF_00218; -; 1.

InterPro; IPR006361; HemE.

InterPro; IPR000257; Uro_decarbxyls.

Pfam; PF01208; URO_D; 1.

ProDom; PD003225; Uro_decarbxyls; 1.

PTIGRFAMs; TIGR01464; hemE; 1.

PROSITE; PS00906; UROD_1; 1.

PROSITE; PS00907; UROD_2; FALSE_NEG.

LYASE; Decarboxylase; Porphyrin_biosynthesis; Comp. SEQUENCE 333 AA; 37785 MW; 3DBE510768COFF5B CR
 CHAIN
DISULFID
SEQUENCE
 16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Uroporphyrinogen decarboxylase (EC 4.1.1.37)
HEME OR TA0310.
 use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and an account is in no entities requires a license secret.
 Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasma
Thermoplasmataceae; Thermoplasma
 Complete proteome.
SIGNAL 1
 Outer membrane; Transmembrane; Fimbria; Transport; Signal
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 Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
 Q9HLB9;
16-ОСТ-2001
 entities requires a license agreement (Some send an email to license@isb-sib.ch).
 STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
 NCBI_TaxID=2303;
 Nature 407:508-513(2000).
-!- CATALYTIC ACTIVITY: Uroporphyrinogen-III
 SEQUENCE FROM N.A.

 -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 -!- SIMILARITY: BELONGS TO THE UROPORPHYRINGEN DECARBOXYLASE FAMILY.

 PATHWAY: Porphyrin biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (Probable)
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 Score 43; DB 1;
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 Hypothetical protein; Outer membrane; Transmembrane; Fimbria; Transport; Signal; Complete proteome.

SIGNAL 1 35 POTENTIAL.
CHAIN 36 866 HYPOTHETICAL OUTER MEMBRANE USHER
 "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage me DNA Res. 3:137-155(1996).

-i- FUNCTION: COLLD BE INVOLVED IN THE EXPORT AND ASSEMBLY PUTATIVE YCBQ FIMERIAL SUBUNIT ACROSS THE OUTER MEMBRAN-1- SUBCELLULAR LOCATION: Integral membrane protein. Outer
 STRAIN=K12 / MG1655;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose L
Mau B., Shao Y.;
 SEQUENCE
 EMBL; AE000196; AAC74026.1; -.
EMBL; D90732; BAA35695.1; -.
PIR; C64834; C64834.
 Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 01-NOV-1997
01-NOV-1997
 EMBL; D90732; BAA35695.1; -.
PIR; C64834; C64834.
EcoGene; EG13711; ycbS.
InterPro; IPR000015; Fimb_usher.
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Yano M., Horiuchi T.;
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 MEDLINE=97061202; PubMed=8905232;
 SEQUENCE FROM N.A.
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 SEQUENCE FROM N.A.
 Enterobacteriaceae;
 Bacteria; Proteobacteria;
 Escherichia coli
 16-OCT-2001
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 complete genome sequence of Escherichia coli K-12."; nce 277:1453-1474(1997).
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 Gammaproteobacteria; Enterobacteriales;
 Score 43; DB
Pred. No. 17;
6; Mismatches
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SEQUENCE 293
 STRAIN=CO-92 / Biovar Orientalis;

MEDLINB=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.N.

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plagu
 15-SEP-2003 (Rel. 42, Last sequence update)
Transcriptional regulator hdfR (H-NS-depdendent HDFR OR YPO3904 OR Y0332.
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STRALM=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz
Fetherston J.D., Lindler L.E., Brubaker R.R., Pla
 EMBL; AJ414159; CAC93370.1;
EMBL; AE013633; AAM83923.1;
PIR; AF0475; AF0475.
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 "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
-!- FUNCTION: Negatively regulates the trainmaster operon fihbc by binding to the underson fib. similariani.
 PRINTS; PR00039; HTHLYSR. PROSITE; PS00044; HTH_LYS
 Straley S.C.,
 HAMAP; MF_01233; -;
 modified
 Nature 413:523-527(2001).
 SEQUENCE FROM N.A.
 Enterobacteriaceae;
 Bacteria; Proteobacteria;
 28-FEB-2003
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PF03466; LysR substrate; 1.
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. 42, Last
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Q1-NOV-1997
 CHAIN
ACT_SITE
SEQUENCE
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
 galactoside galactohydrolase).
Coffea arabica (Coffee).
 InterPro; IPR002241; Glyco_hydro_
InterPro; IPR000111; Glyco_hydro_
Pfam; PF02065; Meliblase; I.
 entities requires a license agreement (Some send an email to license@isb-sib.ch).
 SIGNAL
 Hydrolase;
 PRINTS; PR00740; GLHYDRLASE27.
ProDom; PD002572; Glyco_hydro_GHD; 1.
PROSITE; PS00512; ALPHA_GALACTOSIDASE;
 EMBL; L27992; AAA33022.1; -. PIR; T50781; T50781.
 Gene 140:227-231(1994)
 alpha-galactosidase."
 Zhu A., Goldstein
 MEDLINE=94193002; PubMed=8144030;
 SEQUENCE FROM N.A.,
 NCBI_TaxID=13443;
 Coffea
 Alpha-galactosidase
 "Cloning and functional expression of a
 FUNCTION: PREFERENTIALLY CLEAVES ALPHA-1,3 AND ALPHA-1,4 GLYCOSIDE LINKAGES. INVOLVED IN THE HYDROLYSIS OF THE GALACTOMANNAN, IT SPLATTS ALPHA-LINKED GALACTOSE MOLETIES. IT IS PARTICULARLY SULTABLE FOR THE HYDROLYSIS OF GUAR GUM TO A GUM WITH IMPROVED GELLING PROPERTIES. CAN CLEAVE TERMINAL ALPHA-1,3-LINKED GALACTOSE RESIDUES RESPONSIBLE FOR BLOOD GROUP B SPECIFICITY FROM THE SURFACE OF EXYTHROCYTES THEREBY CONVERTING THESE CELLS SEROLOGICALY TO GROUP O.
 CATALYTIC ACTIVITY: Melibiose + H(2)O = galactose + glucose. SIMILARITY: BELONGS TO FAMILY 27 OF GLYCOSYL HYDROLASES.
 216
 Similarity 6; Conserv
 DKWASYAGPGGWN 228
 DKWEAYITPGAFD 13
 16
287
378
 Glycosidase; Signal.
 (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 39, Last annotation update)
 (Rel.
 Conservative
 AA;
 STANDARD;
 STANDARD;
 14,
14,
 AND
 41310
 51.2%;
 Created)
Last seq
 SEQUENCE
 MW;
 sequence update)
 hydro_GHD
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 Score 41; DB Pred. No. 17; 3; Mismatches
 ALPHA-GALACTOSIDASE.
POTENTIAL.
; 9FC7610BFD760AE3 CRC64;
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 16-34;
 378
 411
 DB
17;
 (See http://www.isb-sib.ch/announce/
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 cDNA encoding
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 215-231
 (Melibiase) (Alpha-D-
 4.
 Length 378;
 Indels
 AND
 Tracheophyta;
 coffee bean
 EMBL outstation
 a collaboration
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 commercial
 8
 0
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RESULT 8
YRS7_CAEEL
ID YRS7_CAEEL
AC Q10003;

STANDARD;

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á
밁
 Query Match
Best Local
 Matches
 CARBOHYD
CARBOHYD
CARBOHYD
ACT SITE
SEQUENCE
 "Messenger RNA from isolated aleurone cells dire an alpha-galactosidase found in the endosperm du guar (Cyamopsis tetragonaloba) seed."; Plant Mol. Blol. 11:783-789(1988).

-i- FUNCTION: INVOLVED IN THE HYDROLYSIS OF THE SPLITS ALPHA-LINKED BALACTOSE MOIETIES. IT I SULTABLE FOR THE HYDROLYSIS OF GUAR GUM TO A GELLING PROPERTIES. PREFERENTIALLY CLEAVES A
 PRINTS; PRO0740; GLHYDRLASE27.
ProDom; PD002572; Glyco_hydro_GHD; 1.
PROSITE; PS00512; ALPHA_GALACTOSIDASE; 1.
Hydrolase; Glycosidase; Signal; Glycoprotein.
 PIR; S07472; S07472.
InterPro; IPR002241; Glyco_hydro_27.
InterPro; IPR000111; Glyco_hydro_GHD.
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 Verrips C.T.; "Cloning and nucleotide sequence of the alpha-galactosidase cDNA from Cyamopsis tetragonoloba (guar)."; Plant Mol. Biol. 13:541-550(1989).
 galactoside galactohydrolase).
(Cyamopsis tetragonoloba (Guar) (Cluster bean).
(Cyamopsis tetragonoloba (Guar) (Cluster bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eurosids; core eudicots; Rosidae;
Eurosids I; Fabales; Fabaceae; Papilionoideae; Indigofereae;
 01-NOV-1997 (Rel. 35, Last annotation update) Alpha-galactosidase precursor (EC 3.2.1.22)
 EMBL; X14619; CAA32772.1;
 or send an email to license@isb-sib.ch).
 Hughes S.G.,
 MEDLINE=91370836; PubMed=2577496;
Overbeeke N., Fellinger A.J., Toonen M.Y., van Wassenaar
 CHAIN
 SIGNAL
 Pfam; PF02065; Melibiase;
 TISSUE=Seed;
 SEQUENCE OF
 SEQUENCE FROM N.A.
 NCBI_TaxID=3832;
 SIMILARITY:
 CATALYTIC ACTIVITY:
 LINKAGES.
 1 DKWEAYITPGAFD 13
 Similarity 6; Conserv
 Ν.,
 DKWASYAGPGGWN
 25
48
32
145
319
 48-57
 Conservative
 Overbeeke N.,
 A,
 BELONGS
 AND 172-178.
 45135
 51.2%;
46.2%;
 Melibiose + H(2)O = galactose + glucose
TO FAMILY 27 OF GLYCOSYL HYDROLASES.
 W.
 .'
 Robinson S.,
 ű,
 ALPHA-GALACTOSIDASE.
N-LINKED (GLCNAC...
 Score 41;
 N-LINKED
 POTENTIAL
 5B1715858D1AB11E
 No.
 S., Pollock K., Smeets F.L.M.; ne cells directs the synthesis of endosperm during germination during germinati
 It is produced through
 (GLCNAC. .
 (See http://www.isb-sib.ch/announce/
 1;
 (Melibiase) (Alpha-D-
 HE GALACTOMANNAN, IT
T IS PARTICULARLY
O A GUM WITH IMPROVED
S ALPHA-1,6 GLYCOSIDE
 Length 411;
 CRC64;
 (POTENTIAL)
(POTENTIAL)
 restrictions
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 EMBL
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 Gaps
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RESULT
FIMD_SA
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 SQUETTINE
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 Query Match
Best Local S
Matches 6
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SETRAIN=LT2 / SGSC1412 / ATCC 700720;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MCDLEIME 21.34948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
MCClelland M., Sanderson K.E., Dieth M., Du F., Hou S., Layman D.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Rvan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 01-OCT-1996
01-OCT-1996
30-MAY-2000
 EMBL; Z47bll, _
PIR; T23238; T23238.
PIR; T23238; T23238.
 SEQUENCE FROM N.A.

Swenson D.L., Clegg S.;

Wenson D.L., Clegg S.;

"The complete nucleotide sequence of a Salmonella typhimurium fimbrial gene cluster.";

Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
 P37924;
01-OCT-1994
 FIMD
 SALTY
 SEQUENCE
 EMBL; Z47811; CAA87788.1; JOINED.
EMBL; Z47812; CAA87788.1; JOINED.
EMBL; Z47812; CAA87796.1; -.
EMBL; Z47811; CAA87796.1; JOINED.
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 Lightning J., Thomas K.; Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
 SEQUENCE FROM N.A.
STRAIN=Bristol N2;
 Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
 Salmonella typhimurium.
 Outer membrane usher protein
 InterPro; IPR004129; GDPD. Pfam; PF03009; GDPD; 1.
 Enterobacteriaceae;
 28-FEB-2003
28-FEB-2003
 DOMAIN
 DOMAIN
 NCBI_TaxID=6239;
 NCBI_TaxID=602;
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 FIMD OR STM0546
 Hypothetical
DOMAIN
 Hypothetical
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 SALTY
 163
 6; Conserv
 DKWEAFLHP
 DKWEAYITP
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ane usher protein fimD precursor.
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(Rel.
(Rel.
1 90.8
 Conservative
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527
 CE03637.
 Salmonella
 90831 MW;
 51.2%;
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Last sequence update)
Last annotation update)
protein T05H10.7 in chromosome
 Score 41; DB Pred. No. 33; 2; Mismatches
 POLY-GLU.
 POLY-GLU.
; 7BDF8E0A4D2AA9F1 CRC64;
 PRT;
 870
 DB 1;
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 Length 796;
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 a collaboration -
 0;
 type
 Gaps
 0;
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DP03
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 RESULT 10
 Query Match
Best Local S
Matches 5
 DPO3 LISIN
Q92C34;
28-FEB-2003
28-FEB-2003
28-FEB-2003
"Comparative year. Science 294:849-852(2001).
Science 294:849-852(2001).
-!- FUNCTION: Required for replicative DNA synthesis.
-!- FUNCTION: Required for replicative DNA synthesis.
 Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Bntian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
 DISULFID
CONFLICT
CONFLICT
 STRAIN=CLIP 11262 / Serovar 6a;
MEDLINE=21537279; PubMed=11679669;
 LISIN
 SEQUENCE FROM N.A.
 Bacteria; Firmicutes; NCBI_TaxID=1642;
 DNA polymerase III POLC OR LIN1357.
 SEQUENCE
 SIGNAL
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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 Nature 413:852-856(2001).
 Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
 CHAIN
 Outer membrane; Transmembrane;
 StyGene; SG10505;
 EMBL; AE008721; AAL19500.1; -.
 EMBL; L19338; AAA75419.1; -.
 Listeria innocua.
 Complete
 Pfam; PF00577;
 -!- SIMILARITY: BELONGS
 PROSITE; PS01151; FIMBRIAL_USHER;
 nterPro;
 FUNCTION: INVOLVED IN THE EXPORT AND SUBUNITS ACROSS THE OUTER MEMBRANE. SUBCELLULAR LOCATION: Integral membra
 (By similarity)
 310
 Similarity 5; Conserv
 proteome.
 YQSYVSPGAFAI 321
 WEAYITPGAFDV 14
 IPR000015; Fimb_usher
 870
 (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
se_III polC-type (EC 2.7.7.7) (PolIII)
 (Rel. 41, Created)
 Conservative
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 Usher; 1
 STANDARD;
 E imb
 27
870
865
265
361
 50.0%;
 95127
 Bacillales; Listeriaceae; Listeria
 TO THE FIMBRIAL EXPORT USHER FAMILY
 3
 Score 40;
Pred. No.
 Pred. No. 53;
6; Mismatches
 V -> F (IN REF. 1).
G -> A (IN REF. 1).
; A6B000139F654A29
 POTENTIAL
 OUTER MEMBRANE
 POTENTIAL.
 PRT;
 ER; 1.
Fimbria; Transport;
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RESULT 11
DPO3_LISMO
 Matches
 Query Match
Best Local
 HAMAP; MF 00336; -; 1.

HAMAP; MF 00336; -; 1.

InterPro; IPR006054; DnaQ.

InterPro; IPR006055; Exonuclease.

InterPro; IPR006055; Exonuclease.

InterPro; IPR0063141; PHP N.

InterPro; IPR0063108; PolC gram pos.

InterPro; IPR006308; PolC gram pos.

InterPro; IPR0064365; TRNA_anti.

Pfam; PF00929; Exonuclease; 1.

Pfam; PF00929; Exonuclease; 1.

Pfam; PF00231; PHP C; 1.

Pfam; PF01316; TRNA_anti; 1.

SMART; SM00481; POLIIIAC; 1.

SMART; SM00481; POLIIIAC; 1.
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Darwara A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 DPO3 LISMO
Q8Y7G1;
28-FEB-2003
 EMBL;
 TIGREAMS; TIGRO1573; dnaq; 1.
TIGREAMS; TIGRO1405; polC Gram pos; 1.
Transferase; DNA-directed DNA polymerase;
Nuclease; Exonuclease; Complete proteome.
DOMAIN 428 592 EXONUCLEASE.
 PIR; AD1602; AD1602.
ListiList; LIN01357; -.
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 STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
 DNA polymerase
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28-FEB-2003 (Rel. 41,
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 SEQUENCE FROM N.A
 Bacteria; Firmicutes;
 Listeria monocytogenes
 CBI_TaxID=1639;
 similarity).
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 SUBCELLULAR
SIMILARITY:
 SUBFAMILY.
 460
 AL596168; CAC96588.1; -.
 Similarity 7; Conserv
 DKWEAYITPG
 DKFEAFIDPG
 1444 AA;
 Conservative
 ACTIVITY: N
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el. 41, Last annotation update)
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 STANDARD;
 LOCATION:
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 deoxynucleoside triphosphate = N diphosphate
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 Score 40;
Pred. No.
 PRT;
 Mismatches
 D4B78BCA39D9AD95 CRC64;
 Listeriaceae; Listeria
 It is produced through
 1444
 (By similarity)
 (See http://www.isb-sib.ch/announce/
 B5;
 DNA replication; Hydrolase;
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ID PHLC BACCE
AC P09508;
DT 01-MAR-1
DT 28-FEB-2
DT 28-FEB-2
DE cholinep
GN PLC.
OS Bacillus
OC NCBI Tax
RN [1]
RP SEQUENCE
RC STRAIN-S
RX MEDLINE
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 Query Match
Best Local S
Matches 7
 Pfam; PF00929; Exonuclease; 1.
Pfam; PF02231; PHP C; 1.
Pfam; PF01231; PHP N; 1.
Pfam; PF01336; tRNA anti; 1.
SMART; SM00479; EXOTII; 1.
SMART; SM00481; POLIIIAC; 1.
TIGRFAMs; TIGR05573; dnag; 1.
TIGREAMs; TIGR05573; dnag; 1.
TIGREAMs; TIGR01405; polC Gram pos; 1.
TIGREAMs; TIGR01405; polC Gram pos; 1.
TYANGEREAMS; TONA-directed DNA polymerase; DN
Nuclease; Exonuclease; Complete proteome.
 EMBL; AL591978; CAC99398.1; -.
PIR, AH1239; AH1239.
ListiList; LM001320; -.
HAMAP; MF 00356; -; 1
InterPro; IPR006054; DnaQ.
InterPro; IPR006055; Exonuclease.
InterPro; IPR004013; PHP C.
InterPro; IPR004131; PHP N.
InterPro; IPR004314; PHP N.
InterPro; IPR004363; ENAB. anti.
InterPro; IPR004365; ERNA anti.
 Vazquez-Boland J.-A., Voss H., Wehland J., Cossart r.;
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
-!- FUNCTION: Required for replicative DNA synthesis.
nolymerase also exhibits 3' to 5' exonuclease acti
 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence upd
28-FEB-203 (Rel. 41, Last annotation u
Phospholipase C precursor (EC 3.1.4.3)
cholinephosphohydrolase) (Cereolysin A)
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MEDLINE=88313678; PubMed=3137122;
Johansen T., Holm T., Guddal P.H.,
"Cloning and sequencing of the gene
preferring phospholipase C of Bacil
Gene 65:293-304(1988).
 or send an email to license@isb-sib.ch).
 -!- CATALYTIC ACTIVITY: N deoxynucleoside
 Bacillus cereus.
Bacteria; Firmicutes;
 SEQUENCE
 DOMAIN
 STRAIN=SE-1;
 SEQUENCE FROM N.A.
 NCBI_TaxID=1396;
 SUBCELLULAR LOCATION: O
 SUBFAMILY.
 BACCE
 460
 DNA (N)
 Similarity 7; Conserva
 DKWEAYITPG
 1444
 Conservative
 STANDARD;
 <u>چ</u>
 592
 10
 50.0%;
 162732
 Bacillales; Bacillaceae; Bacillus
 Cytoplasmic (By similarity)
THE DNA POLYMERASE TYPE-C
 al P.H., Sletten K., Ha the gene encoding the of Bacillus cereus.";
 W.
 2;
 Score 40; DB Pred. No. 85; 2; Mismatches
 EXONUCLEASE
 D8B3F57FBDF3815B CRC64;
 on update)
(3) (PLC)
 283
 (See http://www.isb-sib.ch/announce/
 B
 DNA
 triphosphate = N diphosphate
 1;
 (Phosphatidylcholine
 replication; Hydrolase;
 1;
 Haugli F.B., Little C., he phosphatidylcholine-
 Length 1444,
 sis. This activity
 Indels
 FAMILY.
 restrictions
 and
 EMBL
 DNA
(By
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 Date
 collaboration
 outstation
 Gaps
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12)
SEQUENCE FROM N.A.
SERAIN=VKM B-164;
STRAIN=VKM B-164;
MEDLINE=93249510; PubMed=8387306;
Kuzmin N.P., Gavrilenko I.V., Krukov V.M., I
"Nucleotide sequence of phospholipase C and from Bacillus cereus BKM-B164 (letter).";
Bioorg. Khim. 19:133-138(1993).
 EMBL; X64141; CAA45502.1; -.
EMBL; X12854; CAA31332.1; -.
EMBL; X12711; CAA31213.1; -.
EMBL; X46140; CAA45501.1; ALT_TERM.
PIR; X68978; PS0197
PDB; 1AH7; 10-DEC-97.
InterPro, IPR001531; Zn_dep_PLPC.
PROSITE; PS00384; I
Hydrolase; Zinc; Si
SIGNAL 25
CHAIN 25
METAL 39
METAL 93
METAL 107
METAL 156
METAL 156
METAL 166
METAL 166
METAL 166
METAL 166
METAL 166
METAL 184
 Nature 338:357-360(1989).
-!- FUNCTION: REQUIRED, WITH SPHINGOMYELINASE
-!- CATALYTIC ACTIVITY: A phosphatidylcholine
diacylglycerol + choline phosphate.
 "Some characteristics of phospholipase C
Eur. J. Biochem. 79:459-468(1977).
[5]
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 "Nucleotide sequence and expression in Ecoding for sphingomyelinase of Bacillus Eur. J. Biochem. 175:213-220(1988).
 MEDLINE=89159438; PubMed=2493587;
Hough E., Hansen L.K., Birknes B.
 Otnaess A.-B., Little C
Flengsrud R., Prydz H.;
 MEDLINE=88296483; PubMed=2841128;
Yamada A., Tsukagoshi N., Udaka S.,
Little C., Tomita M., Ikezawa H.;
 SEQUENCE OF 166-283
STRAIN=IAM 1208;
 Prodom; PD003946; Zn_dep_PLPC; PROSITE; PS00384; PROKAR_ZN_DE
 Pfam; PF00882; Zn dep PLPC; 1.
PRINTS; PR00479; PRPHPHLPASEC.
 Bacillus cereus.",
 Hough E., Hansen L.K., Birknes B., Jynge K., Hansen S., Hordvi
Little C., Dodson E., Derewenda Z.;
"High-resolution (1.5 A) crystal structure of phospholipase C
 X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS)
 MEDLINE=78043154; PubMed=72664;
 SEQUENCE OF 39-65.
 diacylglycerol + cholin
COFACTOR: Binds 3 zinc
 SUBUNIT: Monomer.
SIMILARITY: BELONGS
 FAMILY
 Signal;
 24
38
283
39
52
52
107
156
166
180
 FROM
 С.,
 TO THE
 N.A.
 ZN DEPEND PLPC; 1.
Zymogen; Hemolysis;
 Sletten
 ions.
 PHOSPHOLIPASE (
ZINC 3.
ZINC 3.
ZINC 1.
ZINC 1.
ZINC 1.
ZINC 1.
ZINC 1.
ZINC 2.
ZINC 2.
ZINC 2.
 POTENTIAL.
 Krukov V.M., Karpov A.V.;
 BACTERIAL
 K., Wallin
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 01-FEB-1994
01-FEB-1994
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 PHLD BACCE
P33376;
 comprises the phospholipase C an sequence and genetic linkage."; J. Bacteriol. 171:744-753(1989).
 SEQUENCE OF 50-142 FROM N.A.

Gilmore M.S., Gilmore K.S., Goebel W.;

"A new strategy for ordered DNA sequencing based on the rapid purification of near-milligram quantities
 sequence and J. Bacteriol.
 MEDLINE=89123149; PubMed=2536680; Gilmore M.S., Cruz-Rodz A.L., Lei
 Bacillus cereus.
Bacteria; Firmicutes;
 Goebel
 STRAIN=GP-4;
 SEQUENCE FROM N.A
 NCBI_TaxID=1396;
 cholinephosphohydrolase) (Cereolysin
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RESULT 14
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 EMBL; M24149; AAA71611.;
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 the European Bioinformatics Institute. There are no restriuse by non-profit institutions as long as its content imodified and this statement is not removed. Usage by and
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S-adenosylmethionine:tRNA ribosyltransferase-isomerase
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PRODOm; PD003946; Zn_dep_PLPC; 1.
PROSITE; PS00384; PROKAR_ZN_DEPEND_PLPC; 1.
Hydrolase; Zinc; Signal; Zymogen; Hemolysis.
 entities requires a license agreement (Some send an email to license@isb-sib.ch).
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EV
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 Gene Anal.
 Nierman W.C., Feldblyum T.V., Laub M.T., Paul
Eisen J., Heidelberg J.F., Alley M.R.K., Obte
Potocka I., Nelson W.C., Newton A., Stephens
DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn N
 SEQUENCE FROM N.A.
STRAIN=ATCC 19089
MEDLINE=21173698;
 (Queuosine biosynthesis protein queA) QUEA OR CC1587.
 SEQUENCE
 NCBI_TaxID=155892
 Caulobacteraceae;
 Bacteria; Proteobacteria;
 Caulobacter crescentus
 I- FUNCTION: REQUIRED, WITH SPHINGOMYELINI
LYSIS (HEMOLYSIS).
I- CATALYTIC ACTUVITY: A phosphatidylcholi
diacylglycerol + choline phosphate.
I- COPACTOR: Binds 3 zinc ions.
I- SUBULIARITY: BELONGS TO THE BACTERIAL ZI
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llarity 66.7%;
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9089 / CB15;
698; PubMed=11259647;
Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson Feldblyum T.V., Laub M.R.K., Ohta N., Maddock J.R.
delberg J.F., Alley M.R.K., Ohta N., Maddeck J.R.
Ldelberg J.F., Nawton A., Stephens C., Phadke N.D.,
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 acteria; Alphaproteobacteria;
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 Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Ber Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; "Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

-i- FUNCTION: Synthesizes oQ from preQ1 in a single S-adenosylmethionine-requiring step. The ribosyl molety of transferred and isomerized to the epoxycyclopentane residence.
 Pfam; PF02547; Queuesine synth; TIGRFAMs; TIGR00113; queA; 1. Queuesine biosynthesis; Transfer SEQUENCE 366 AA; 39817 MW; F
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entrepean Bioinformatics Institute. There are no restrues by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
 Storey C.C., Lusher M., Richmond S.J.
"Analysis of the complete nucleotide
infects avian Chlamydia psitraci.";
J. Gen. Virol. 70:3381-3390(1989).
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 pfam; PP02305; Phage F; 1.
Structural protein
 Bacteriophage Chpl.
Viruses; Microviridae; Microvirus
 HAMAP; MF_00113; -; 1 InterPro; IPR003699;
 EMBL; AE005833; AAK23566.1; -.
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 NCBI_TaxID=12367;
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 PATHWAY: Queuosine biosynthesis
SUBCELLULAR LOCATION: Cytoplasmi
SIMILARITY: BELONGS TO THE QUEA
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Search completed: January 12, 2004, 06:59:39 Job time : 10.6582 secs	Qy	Query Match Best Local Similarity 60.0%; Pred. No. 55; Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Title:
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 Post-processing: Minimum Match 0%
Maximum Match 100%
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 January 12, 2004, 06:54:04; Search time 28.4375 Seconds (without alignments) 127.041 Million cell updates/sec
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 1 DKWEAYITPGAFDV 14
 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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 human:*
 830525
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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Strapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Strapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise B.,
George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
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Miranda A., Mungall C.J., Nunoo J., Pacleb J., Lewis S.E., Rubin G.M.
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

Wan K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,

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Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

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 Neoptera, Endopterygota; Diptera; Brachycera; Ephydroidea; Drosophilidae; Drosophila. NCBI TaxID=7227;
 BRN OR EG:EG0007.6 OR CG4934.
Drosophila melanogaster (Fruit f
Eukaryota; Metazoa; Arthropoda;
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 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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RA Sylerkas R., Tector C., Turner R., Venter E., Mang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wang A.H., Wang X.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RD RHBL, AR003430; AAP45918.1; -.

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 urosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI TaxID=7227;
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MEDLINE=20196011; PubMed=10731137;
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J.,
Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolsh
 "The neurogenic genes pathway essential for oogenesis.";
 MEDLINE=97164700; Pub
Goode S., Melnick M.,
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 122:3863-3879(1996).
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Delcher A.,
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 pubMed=9012507;
M., Chou T.-B., Perrimon N.;
enes egghead and brainiac define a novel signaling
for epithelial morphogenesis during Drosophila
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A Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

A Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

A Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

A Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

A McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.

A McDonald L.A., Feldblyum T.V., Smith H.O., Venter J.C.,

A Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

T "Complete genome sequence of a virulent isolate of Streptococcus

T pneumoniae.";

Science 293:498-506 (2001).
 PROSITE;
Complete
 CONFLICT
 Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F., Beinert N., Dowe G., Schaefer U., Jackle H., Bucheton A., Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S., McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D. Glover D.M.;
 SP2157.
Streptococcus
 01-OCT-2001
01-DEC-2001
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 FlyBase; FBgn0000221; brn.
InterPro; IPR002659; Glyco_trans_31.
Pfam; PF01762; Galactosyl_T; 1.
 InterPro; IPR001670; Fe-ADH.
Pfam; PF00465; Fe-ADH; 1.
PROSITE; PS00913; ADH IRON 1;
PROSITE; PS00060; ADH IRON 2;
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 Alcohol dehydrogenase, iron-containing
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 melanogaster."
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 NCBI_TaxID=1313;
 Streptococcus.
 Bacteria;
 SEQUENCE
 "From sequence to chromosome: the tip of the X chromosome of
 Papagiannakis G., Spanos
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 ENCE 287:2220-2222(2000).

FUNCTION: NEUROGENIC PROTEIN ESSENTIAL FOR THE DEVELOPMENT AND MAINTENANCE OF EPITHELIAL STRUCTURE. REQUIRED IN THE GERMLINE E ESTABLISHING THE FOLLICULAR EPITHELIUM AND FOR DETERMINING THE EDRSAL-VENTRAL POLARITY. COLLABORATES WITH NOTCH ON THE APICAL SURFACE OF FOLLICLE CELLS TO MEDIATE GERMLINE-FOLLICLE CELL
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 MEDLINE=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett & Hoskins J., Alborn W.F., Fritz L., Fu D.-J., Fuller W., Geringe: DeHoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringe: Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Nortis F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud I
 Hosouchi T.
Shimpo S.,
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EMBL; AE008560; AAL00765.1; -
Oxidoreductase; Complete proteome.
SEQUENCE 383 AA; 41154 MW; 8E181FCD5A168B4B
 Synechocystis sp. entire genome and
 Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
NCBI_TaxID=1148;
 Hypothetical SLR1567.
 P74599;
01-FEB-1997
 P74599
 Glass J.I
 Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcac
 Probable alcohol dehydrogenase (EC ADH2 OR SPR1963.
 "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
 Tabata S.;
 Miyajima
 SEQUENCE FROM N.A.
MEDLINE=97061201; PubMed=8905231;
 01-MAR-2002
 01-FEB-1997
 Kaneko
 SEQUENCE
 NCBI_TaxID=171101;
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 i T., Marchi
S., Takeuchi
 Similarity 72.8
8; Conservative
 Similarity
 ., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okum T., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda
 FROM N.A.
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 nome and assignment 3:109-136(1996).
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SEQUENCE 76
 01-NOV-1998
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 080091;
MEDLINE=98332719; PubMed=9666077; Kaneko J., Kimura T., Narita S., Tomita T., Kamio Y.; Kaneko J., Rimura T., Narita S., Tomita T., Kamio Y.; Complete nucleotide sequence and molecular characterization of temperate staphylococcal bacteriopbage phi PVL carrying Panton-valentine leukocidin genes."; Gene 215:57-67(1998).
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Stapplylococcus aureus P83 is linked with lukM.";
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 Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AF424781; AAL82253.1; -. InterPro; IPR001428; DeoxyUTPase.
 SEQUENCE
 Viruses
 DUTPase.
 01-JUN-2002
01-JUN-2002
 Q8SDV3;
 Q8SDV3
 Staphylococcus aureus bacteriophage PVL.
Viruses, dsDNA viruses, no RNA stage; Ca
 TIGRFAMS; TIGR00576; dut; 1. SEQUENCE 169 AA; 18369 MW;
 "Comparative analysis of the genomes of the #11, #12 and #13 of Staphylococcus aureus
 Jia H.;
 NCBI_TaxID=12360;
 Bacteriophage phi-11.
 01-OCT-2002
 NCBI_TaxID=71366;
 Pfam; PF00692; dUTPase; 1.
ProDom; PD000946; DeoxyUTPase; 1.
 Iandolo J.J., Worrell V.,
 SEQUENCE FROM N.A.
 MEDLINE=98067870; PubMed=9404084;
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CG4704 protein.
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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ProDom; PD000946; DeoxyUTPase; 1.
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 MEDLINE=96154943; PubMed=8596463;
Bruton C.J., Plaskitt K.A., Chater K.F.;
"Tissue-specific glycogen branching isoenzymes in prokaryote, Streptomyces coelicolor A3(2).";
Mol. Microbiol. 18:89-99(1995).
EMBL; AJ001206; CAA04606.1; -.
InterPro; IPR000539; Actbind_actnin.
InterPro; IPR000531; TonB_boxC.
InterPro; IPR000531; TonB_boxC.
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 EMBL; AEDU3/90; CO. FlyBase; FEgn0039029; CG4704. InterPro; IPR002048; EF hand.
 Q9KY04
 MEDLINE=20279210; PubMed=10821190; Schneider D., Bruton C.J., Chater K.F.; Schneider D., Bruton C.J., Chater K.F.; "Duplicated gene clusters suggest an interplay of glycogen and trehalose metabolism during sequential stages of aerial mycelidevelopment in Streptomyces coeli color A3(2)."; Mol. Gen. Genet. 263:543-553(2000).
 Pfam; PF00036; efhand; 2.
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 Bacteria; Actinobacteria;
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 Eukaryota;
Mammalia; E
 PRP3.
 Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harris D.E., Quail M.A., Kieser H., Collins M., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 EMBL;
 Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic at the 8 Mb Streptomyces coelicolor A3(2) chromosome.
 U4/U6-associated
 Pfam; PF00128; alpha-amylase; PROSITE; PS00019; ACTININ 1; 1 PROSITE; PS00430; TONB_DEFENDE Complete proteome.
 coelicolor A3(2).";
Nature 417:141-147(2002)
 STRAIN=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
 STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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 Homo sapiens
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 Submitted
 Bacteria; Actinobacteria;
 Streptomyces coelicolor.
 "Complete genome sequence of the model actinomycete Streptomyces
 Hopwood D.A.;
 SEQUENCE FROM N.A.
 Mol. Microbiol. 21:77-96(1996).
 Redenbach M.,
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 Kieser H.M.,
 AA;
 Streptomycetaceae;
 Chordata;
Primates;
 74143 MW;
 87
 55.0%;
63.6%;
 to the EMBL/GenBank/DDBJ databases
 the
 Actinobacteridae; Actirycetaceae; Streptomyces.
 Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
 Denapaite
 Score 44; DB Pred. No. 45; 2; Mismatches
 2
 Catarrhini;
 Craniata; Vertebrata; Euteleostomi;
 5463E0134CD66518 CRC64;
 Ð.,
 682
 genetic and
 B
 Eichner
 Hominidae;
 16;
 Actinomycetales;
 update)
 Length 669;
 Α.,
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 Cullum J.,
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 Gaps
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OPD6C6
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OA 3446
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 RESULT 15
 Query Match
Best Local S
Matches 6
 Matches
 Query Match
Best Local :
 SEQUENCE FROM N.A.

MEDLINE=98067393; PubMed=9404889;
Horowitz D.S., Kobayashi R., Krainer A.R.;
Horowitz D.S., Kobayashi R., Krainer A.R.;
TA new cyclophilin and the human homologues of yeast Prp3
form a complex associated with U4/U6 snRNPs.";
RNA 3:1374-1387(1997).
[2]
 Wang A., Forman-Kay J., Luo Y., Luo M., Chow Y.-H., Plumb J., Friesen J.D., Tsui L.-C., Heng H.H.Q., Woolford J.L. Jr., Hu J.; Indentification and characterization of human genes encoding Hprp3p and Hprp4p, interacting components of the spliceosome."; Hum. Mol. Genet. 6:2117-2126(1997).

EMBL; AF001947; AAC09069.1; -.
01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2003 (TrEMBLrel. 23, 3632413F13Rik protein.
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 InterPro; IPR002483; PWI. Pfam; PF01480; PWI; 1. SMART; SM00311; PWI; 1. SEQUENCE 682 AA; 77403
 SMART; SM00311; PWI; 1.
Nucleoprotein; Ribonucleoprotein.
SEQUENCE 683 AA; 77528 MW; 47
 01-OCT-2002
U4/U6 small
 01-JUN-1998
01-JUN-1998
 043446;
 043446
 Q9D6C6;
 Q9D6C6
 InterPro; IPR002483; PWI. Pfam; PF01480; PWI; 1.
 Strausberg R.;
 TISSUE=Skin,
 SEQUENCE FROM N.A.
 MEDLINE=97472464; PubMed=9328476;
 390
 390
 tted (JAN-2001) to the EMI
AF016370; AAC51926.1; -.
BC001954; AAH01954.1; -.
BC000184; AAH00184.1; -.
 l Similarity
6; Conserv
 3 WEAYITPGAFDV 14
 w
 Similarity 6; Conserv
 WDSYIIPNGFDL
 WDSYIIPNGFDL
 WEAYITPGAFDV
 (TrEMBLrel. 06, Created)
(TrEMBLrel. 06, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
nuclear ribonucleoprotein HPRP3 (U4/U6-associated RNA
 Conservative
 Conservative
 PRELIMINARY;
 PRELIMINARY;
 and Eye;
 77403 MW;
 50.0%;
 50.0%;
 401
 14
 401
 Created)
Last sequence update)
Last annotation updat
 3;
 EMBL/GenBank/DDBJ databases.
 Score 44;
Pred. No. 4
 Score 44; DB
Pred. No. 46;
3; Mismatches
 544660BF72A39BA3 CRC64;
 4AA6AA4C99110284 CRC64;
 Mismatches
 683
 683
 DB 46;
 DB 4;
46;
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 4.
 Length 682;
 Length 683
 Indels
 and
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 Prp4
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Search completed: January 12, 2004, 07:02:03 Job time: 33.4375 secs

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 SODRA CORRESPONDE SOR CORRESPO
밁
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X Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

X Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Pukunishi Y., Konno H., Kando S., Yamanaka I.,

X Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

X Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

X Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

X Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

X Fleischmann W., Gaasterland T., Mikaido I., Pesole G., Quackenbush J.,

X Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

X Kuchl P., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

X Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

X Blake J., Boftelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

X Blake J., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

X Blake J., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,

X Blake J., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

X Baski H., Sato K., Schoenbach C., Seya T., Shibata Y., Wilming L.,

X Barchard Y., Waing K.H., Weilt C., Whittaker C., Wilming L.,

X Barchard Y., Weilt C., Wainteker C., Wilming L.,

X Barchard Y., Weilt C., Wandi H., Kohtnuki S.,
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Matches 6
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PROSITE; PS00308; LECTIN LEGUME ALPHA; 1.
SEQUENCE 683 AA; 77430 MW; B1FC8E27DCE3DEFA CRC64;
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 Nature 409:685-690(2001).
EMBL; AK014398; BAB29324.1; -.
MGD; MGI:1918017; 3632413F13R1k.
 Hayashizaki Y.; "Functional annotation of a
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 Conservative
 TISSUE-Brain;
 50.0%;
 <u>ب</u>
 full-length mouse
 Score 44;
Pred. No.
 Mismatches
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 Kawaji H., Kohtsuki S.,
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 Indels
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 Gaps
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 8
 Database :
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 Title:
Perfect score:
 Run on:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 A Geneseq_19Jun03:*

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 January 12, 2004, 06:47:09; Search time 33.9062 Seconds (without alignments) 65.539 Million cell updates/sec
 BLOSUM62
 US-09-829-495-63
80
 1107863 seqs, 158726573 residues
 Gapop 10.0 , Gapext 0.5
 DKWEAYITPGAFDV 14
 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
SUMMARIES
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	44	45	46	46	47	47	52.5	80	80	Score
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100	100	831	383	383	325	193	267	14	14	% Query Match Length DB
-	10	22	24	24	22	23	23	24	22	DB
20004	VEUBCAV	ABG08487	ABU02685	ABP81494	ABB61108	AAE15968	AAU75503	ABU11261	AAB61295	ID
Willing acta seducit		Novel human diagno	S. pneumoniae type	Streptococcus pneu	Drosophila melanog	Fly CP15828/84-303	Human s-acyl fatty	Human TANGO 268 VH	Anti-TANGO 268 scF	Description

45	44	43	42	41	40	39	38	37	36	35		33	32	31	30		28		26				22		20	19	18	17	16	15	14	13	12	11	10
40	40	40	40	40	40	40	40	40	40	41	41	41	41	41	41	41	41	41	41	41	41	41	41	42	42	43	43	43	43	43	43	43	44	44	44
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221	220	220	220	220	117	117	116	93	43	1846	420	411	406	378	378	378	378	363	312	249	245	205	172	243	71	1090	1090	906	424	223	217	207	867	369	354
21	23	23	23	22	15	15	15	22	22	22	16	16	18	23	23	17	16	18	21	23	23	22	22	23	22	22	22	22	22	21	21	21	22	24	22
AAB18667	AAE14361	ABG32808	ABP69836	AAE04837	AAR52067	AAR52065	AAR52061	ABG04397	AAM90168	ABB63163	AAR71326	AAR70206	AAW26604	ABB09593	ABB09592	AAW00621	AAR70205	AAW10320	AAB18153	ABP27381	ABP29803	AAU30764	AAU03641	ABP27382	AA013076	ABG18331	ABG17694	ABG18321	ABG29934	AAG34188	AAG34189	AAG34190	AAG98887	ABU71061	ABB60901
A human regulator	Human dual-specifi	Human Tyrosine spe	Human polypeptide	Human SGP003 phosp	chain	Heavy chain variab	chain	Novel human diagno	Human immune/haema	Drosophila melanog	Coffee bean alpha-	Alpha-galactosidas	Senna alpha-galact	Coffea canephora c		Coffee bean alpha-	Alpha-galactosidas	Soybean alpha-D-ga		Streptococcus poly	Streptococcus poly	Novel human secret	Group B Streptococ	Streptococcus poly	Human polypeptide	Novel human diagno	human	human	el human	ηď	Zea mays protein f	2		Human adipocyte Se	Drosophila melanog

## ALIGNMENTS

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	(MILL-) MILLENNIUM PHARM INC.		14-FEB-2000; 2000US-0503387.		30-JUN-1999; 99US-0345468.		30-JUN-2000; 2000WO-US18152.		04-JAN-2001.		WO200100810-A1.		Homo sapiens.		cancer.	ischaemia; cardiovascular disease; immunological disease; liver disorder;	blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;	platelet membrane glycoprotein receptor; bleeding disorder;	thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;	TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;	Human; antibody; scFv; CDR; complementarity determining region;		Anti-TANGO 268 scFv CDR, SEQ ID NO: 63.		04-APR-2001 (first entry)		AAB61295;		AAB61295 standard; Peptide; 14 AA.	년 1 1 · · · · · · · · · · · · · · · · ·	

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RESULT 2
ABULL 261
ID ABULL
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XX ABULL
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 Matches
 Query Match
 Human; mouse; variable heavy; VH; antigen; cancer; complementarity determining region; TANGO 268; glycoprotein VI; GPVI; TANGO 268; extracellular matrix; collagen; platelet release; proliferation; migration; embryogenesis; inflammation; thrombosis; degranulation; thrombocytopaenia; antibody; thrombotic disorder; cerebral vascular disease; stroke; ischaemia; venous thromboembolism; leg swelling; pain; ulceration; pulmonary embolism; coronary disease; cardiovascular disease; angina pectoris; myocardial infarction; coronary restenosis; atherosclerosis; immunological disorder; developmental disorder; embryonic disorder; liver disorder; cerebral vascular disease; venous thromboembolism disease.
 ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent acture
 nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids,
 New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and disamosing hemorrhagic disorders, thrombotic diseases and
 and diagnosing hemorrhagic immunological disorders -
 Busfield SJ, Ville:
Qian MD, Kingsbury
 09-APR-2001; 2001US-0829495.
 09-APR-2002; 2002WO-US11122
 WO200280968-A1
 Human TANGO
 06-FEB-2003
 ABU11261
 ABU11261 standard; Peptide; 14
 Sequence
 cardiac
 The present
 Claim
 WPI; 2001-080877/09
 (MILL-) MILLENNIUM PHARM INC
 Local
 31;
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 14;
 Similarity
 ischaemia following angioplasty and lly of the colon and liver.
 DKWEAYITPGAFDV 14
 DKWEAYITPGAFDV
 Page 102; 227pp; English
 14
 268 VHCDR3 Peptide #3
 sequence
 Conservative
 Villelal J,
ngsbury G;
 (first entry)
 Å,
 100.0%;
 is given in a specification relating to an isolated
 Jandrot-Perrus M,
 0;
 Score 80;
Pred. No.
 A
 Mismatches
 4.9e-07;
 DB 22;
 are used to prevent acture d metastatic cancers,
 Vainchencker W,
 0
 Length 14;
 0
 Gill DS;
 Gaps.
 0
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Query Match

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24;

Length

0

Sequence

14

A

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CC of very curs; or variable 1910 (very consequence) of immunospecifically binding to a TANGO 268 (also referred as glycoprotein CC vi (GPVI)) antigen. The antibodies of the invention act to decrease or CC block TANGO 268 binding to extracellular matrix components, or as a CC collagen or platelet release and aggregation blocker. The antibodies of the invention are useful for modulating proliferation, migration, CC morphology, differentiation and/or function of megakaryocytes and CC platelets, including during development e.g. embryogenesis, modulating platelets, and platelet-endothelium interactions in modulating lenkocyte-platelet and platelet-endothelium interactions in modulating configuration. They are also useful for modulating platelet aggregation and CC inflammation and/or thrombosis, and modulating platelet aggregation and CC digranulation. They are also useful for modulating disorders associated CC with abnormal or aberrant megakaryocyte and/or platelet proliferation, cm in the context may be constanted by these antibodies are thrombotic disorders, cerebral CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism diseases (e.g. diseases including angina pectoris, myocardial infarction, coronary createnosis, atheroselerosis, etc); immunological disorders, cerebral conductar diseases, venous thromboembolism disease, coronary diseases, cand metastatic cancers. The antibodies of the invention only causes and context for the invention only causes and only causes and context for the invention only causes and only causes and context for the invention only causes and context for the invention only causes and only causes and context for the invention of the invention only causes and only causes and context for the invention of the context of the
 variable heavy (VH) complementarity determining region (CDR); or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3; immunospecifically binding to a TANGO 268 (also referred as
 Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 Busfield SJ, Villeval J, Qian DM, Kingsbury G;
 transient decrease in platelet counts, platelet aggregation, and/or platelet activation and so have some advantages over prior art methods. The present sequence represents a peptide sequence used to
 generate the
 This invention
 Claim
 2003-058477/05
 8
 Page 111;
 antibodies of the invention
 relates to a novel
 236pp; English
 Jandrot-Perrus M,
 purified antibody comprising
 Vainchencker W,
 (CDR) 1,
 ₽a
 Gill DS;
 CDR2
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RESULT 3
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 Best Loc
Matches
 cardiant; anorectic; vasotropic; extracellular matrix degradation; cardiovascular disease; hyperlipidaemia; obesity; anorexia; cachexia; wasting disorder; appetite suppression; appetite enhancement; bulimia diabetes; congestive heart failure; myocardial infarction; human; ischaemic disease; atrial arrhythmia; ventricular arrhythmia;
 S-acyl fatty acid synthase thioesterase-like; SFST-like; enzyme;
 hypertensive
 23-APR-2002
 AAU75503;
 AAU75503 standard; Protein;
 Local
 s-acyl
 14;
 Similarity
 DKWEAYITPGAFDV 14
 Conservative
 vascular disease;
 fatty acid synthase thioesterase-like enzyme
 (first entry)
 100.0%;
 267
 0
 Score 80; DB
Pred. No. 4.9
); Mismatches
 peripheral
 4.9e-07;
 vascular disease
 0
 Indels
 #2.
 0
 bulimia;
 Gaps
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i.

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RESULT 4
AAE15968
ID AAE1
XX
AC AAE1
AC AAE1
AC AAE1
AC AAE1
XX
DT 26-1
XX
DE Fly
KW Fri
KW N-a
KW N-a
KW Dre
KW not
XX
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XX
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 The invention describes a purified human S-acyl fatty acid synthase CC thioesterase (SFST) like enzyme (I) (I) is useful for screening for agents which decrease or regulate the activity of an SFST-like enzyme and CC agents which decrease extracellular matrix degradation. The CC encodes (I) in a biological sample by formation of a hybridisation cC encodes (I) in a biological sample by formation of a hybridisation cC entibody can also be used to detect the polypeptide or polynucleotide in CC antibody can also be used to detect the polypeptide or polynucleotide in CC antibody can also be used to detect the polypeptide or polynucleotide in CC antibody can also be used to detect the polypeptide or polynucleotide in CC antibody can assign a SFST-like enzyme dysfunction related disease condition such as cardiovascular disease, hyperlipidaemia, obesity, CC anorexia, wasting disorders, appetite suppression, appetite condition such as cardiovascular disease, hyperlipidaemia, obesity, CC anorexia, cachexia, wasting disorders, appetite suppression, appetite cCC enhancement, bulimia or diabetes. The cardiovascular diseases treated by the above mentioned methods and reagents include congestive heart CC failure, myocardial infarction, ischaemic diseases of the heart, atrial and contricular arrhythmia, hypertensive vascular diseases, and cCC entipheral vascular diseases. (I) is useful in diagnostic assays for CC detecting diseases and abnormalities related to presence of mutations in CCC acid sequences which encode the enzyme. This is the amino CCC enzyme, described in the method of the invention.
 Best Loca
Matches
 Query Match
Best Local Similarity
 Fringe protein; Brainiac protein; glycosyltransferase; EGF; mannose; N-acetylglucosamine; fucose; epidermal growth factor; T cell leukaemia; breast cancer; stroke; dementia; leucoencephalopathy; Alagille syndrome; notch protein; EGF-module containing protein; fly.
 26-MAR-2002
 Sequence
 New purified human S-acyl fatty acid synthase thioesterase-like enzyme, useful for identifying modulators of enzyme activity for treating cardiovascular disease, diabetes, obesity and hyperlipidaemia -
 Xiao
 26-JUN-2000; 2000US-214012P
14-DEC-2000; 2000US-255148P
 WO200187321-A2
 Drosophila sp.
 Fly CP15828/84-303 protein,
 AAE15968 standard; Protein; 193
 Disclosure; Fig 4; 123pp; English.
 WPI; 2002-130886/17.
 03-JAN-2002
 WO200200855-A2
 26-JUN-2001; 2001WO-EP07297
 (FARB) BAYER
 10;
 44
 DKWEAYITPGAFDV 14
 DRWREY-TPGAFDV 239
 267 AA;
 Conservative
 (first entry)
 ÃG
 65.6%;
 member of Brainiac family
 ۳.
 Score 52.5;
Pred. No. 0.
 Mismatches
 .69;
 23;
 2
 Indels
 Length
 267;
 ۲,
 Gaps
 1;
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RESULT 5
ABB61108
ID ABB6
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 Query Match
Best Local S
Matches 7
 brainiac protein, as glycosyltransferase. Fringe and Brainiac proteins have been found to possess glycosyltransferase activity in transferring sugar residues onto certain proteins of biological transferring sugar residues onto detertain proteins of biological interest, so affecting the binding of effector molecules to these proteins. Particularly they are useful for transferring a N-acetylglucosamine moiety onto a fucose or a mannose substrate, whether free or attached to a lipid, carbohydrate or protein. They are useful for carbohydrate or protein. They are useful in treatment of a disease caused by epidermal growth factor (EGF) like module containing protein, such as T cell leukaemia, breast cancer, stroke, dementia, cerebral autosomal dominant arteriopathy with subcortical infarcts, leucoencephalogathy and Alagille syndrome. Fringe and Brainiac proteins are also useful for screening ligands capable of modulating the activity of the protein. The present sequence is fly protein
 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
 Drosophila melanogaster.
 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
 Drosophila melanogaster polypeptide SEQ ID NO 10116
 26-MAR-2002 (first entry)
 ABB61108;
 ABB61108 standard; Protein; 325 AA
 Sequence
 Claim 7;
 dementia
 Use of Fringe protein or Brainiac protein as glycosyltransferase and treatment of disease caused by epidermal growth factor-like module containing protein, such as T cell leukemia, breast cancer, stroke and
 Cohen S,
 23-MAR-2001; 2001WO-US09231.
 WO200171042-A2
 The invention relates to the use of a Fringe protein protein or a fragment or functional equivalent of a l
 21-MAY-2001; 2001WO-IB01033.
 22-NOV-2001
 19-MAY-2000; 2000GB-0012216
 (EUMO-) EURO MOLECULAR BIOLOGY LAB
 146
 is a member of Brainiac protein family.
 1 DKWEAYITPGAF 12
 Similarity
7; Conserv
 DRWPPYVTAGAF 157
 Fig 1; 52pp; English.
 Brueckner K,
 193 AA;
 Conservative
 58.8%;
 Clausen H,
 Score 47;
Pred. No.
 Mismatches
 Keck
 DB 4.3;
 ₿;
 23; Length 193;
 Indels
 a Fringe
 or a Brainiac
 or a
 0,
 Gaps
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0,

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RESULT 6
ABP81494
ID ABP8
XX ABP8
XX ABP8
XX ABP8
XX ABP
XX Str
X
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 밁
 Query Match
Best Local S
Matches 7
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL/167-ABL/3011), expressed DNA sequences (ABL/1673)-ABL/3017) and the encoded proteins (ABB/7037-ABL/3017).
 genes from Drosophila and interactions -
 Streptococcus pneumoniae; diagnosis; gene therapy.
 The sequence data for this patent did not form specification, but was obtained in electronic f
 Disclosure; SEQ
 Claim 42; Page 680-682; 1091pp;
 New Streptococcus pneumoniae polynucleotides, useful preventing S. pneumoniae infections, or non-systemic otitis media, which are induced or exacerbated by S.
 16-APR-2001;
18-APR-2001;
 Streptococcus pneumoniae
 Streptococcus
 04-MAR-2003
 ABP81494;
 ABP81494 standard; Protein; 383
 (PEKE)
 12-APR-2002; 2002WO-US11524
 WO200283855-A2
 N-PSDB;
 (AMCY
 Mooters
 cification, but was obtained in electronic
ftp.wipo.int/pub/published_pct_sequences.
 2003-093010/08.
DB; ABZ42342.
 2001-656860/75
 229
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 JC,
 l Similarity
7; Conserve
 PE
 у RJ,
JL;
 ABL05211.
 AMERICAN CYANAMID
 DRWPPYVTAGAF 240
 DKWEAYITPGAF
 CORP NY
 325 AA;
 Adams M,
 Conservative
 2001US-283948P.
2001US-284443P.
 pneumoniae
which are i
 pneumoniae polypeptide
 (first entry)
 Masi
 IJ
 AW,
 NO 10116; 21pp + Sequence Listing; English
 58.8%;
 12
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 Green
 PWD,
 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
 ႘
 infection;
 2;
 Score 47; I
Pred. No. 7
 BA,
 Myers
 Mismatches
 English
 Chakravarti
 EW;
 SEQ ID
 otitis
 DB
7.6;
 22;
 media;
 NO 411.
 ω
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 n part of the printed
format directly from
 Ŋ,
 Length 325
 Indels
 antibacterial;
 Russell
 pneumoniae
 diseases, e.
 for treating
 The invention
signalling and
 0;
 Gaps
 ė
 WIPO
 ĺB
 0
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RESULT 7
ABU02685
 *888888888888
S
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 Query Match
Best Local S
 Matches
 The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABP81299-ABP81674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy.
 The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a sequence not defined in the specification, for amplifying a sequence not defined in the specification, for amplifying a
 New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or ear infection -
 Bacterial meningitis; pneumonia; sepsis; otitis ear infection; antiinflammatory; antibacterial;
 Sequence
 N-PSDB;
 Masignani V,
 27-MAR-2001; 2001GB-0007658
 Streptococcus pneumoniae type 4
 auditory;
 11-FEB-2003
 ABU02685;
 ABU02685 standard;
 Claim 1;
 (CHIR-)
 27-MAR-2002; 2002WO-IB02163
 WO200277021-A2
 pneumoniae type
 2003-040579/03.
 199
 4
 8; Conserv
 CHIRON SPA.
INST GENOMIC
 ABX07976.
 SEQ ID
 EALVTPGAYDV
 EAYITPGAFDV 14
 respiratory; gene therapy; vaccine.
 383
 Conservative
 (first
 Tettelin
 A
 ö
 4 strain
 Protein;
 4528;
 entry)
 RES
 209
 57.5%;
72.7%;
 ŗ
 56pp;
 Fraser C;
 protein from coding
 383
 Score 46; DB Pred. No. 13; 2; Mismatches
 2
 English
 strain.
 A
 24;
 ۲,
 Length 383;
 immunostimulant;
 region #2264
 Indels
 0
 infection
 Gaps
 0
```

contained within a

Streptococcus nucleic

8888888888888888888888888888

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RESULT 8
ABG08487
 밁
 Query Match
Best Local S
Matches 8
 genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, particularly S. pneumoniae, such as pneumonia, sepsis, otitis media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the proteins expressed by the identified coding regions from the
 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes polymerase chain reaction (PCR) primers, oligomers, and for chromometers are chain reaction.
 WO200175067-A2
 Novel human diagnostic protein #8478
 13-FEB-2002
 Sequence
 sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more
 Claim 20; SEQ ID No 38846; 103pp; English
 N-PSDB; AAS72674.
 31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
 Homo sapiens
 ABG08487
 genomic sequence.
 sequence and complement of
 30-MAR-2001; 2001WO-US08631.
 11-OCT-2001
 ftp.wipo.int/pub/published_pct_sequences.
 of the printed specification, format directly from WIPO at
 having
 (HYSE-) HYSEQ
 2001-639362/73
 199
 The sequence data for this
 the first primer is substantially complementary to the target toe and the second primer is substantially complementary to the sment of the target sequence, and where the parts of the primers substantial complementarity define the termini of the target
 4 EAYITPGAFDV 14
 RT,
 Similarity
8; Conserv
 standard;
 EALVTPGAYDV 209
 383
 Conservative
 Liu C,
 (first
 INC.
 A,
 Protein;
 entry)
 57.5%;
 Tang
 ΤY
 831
 2
 Score 46; DB
Pred. No. 13;
 but
 Mismatches
 patent did not form
 was
 obtained
 24;
 1;
 ij
 Length 383;
 Indels
 electronic
 part
 mutations
 0
 Gaps
 0
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S

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RESULT 9
AAW28034
ID AAW2
XX AAW2
AC AAW2
XX AAW1
AC AAW2
XX Stag
XW Stag
XW Stag
XW Vacc
XW Vacc
XW Vacc
XW VO97
XX 19-1
XX 1
 S
 밁
 and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human cations canino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
 Matches
 Best Local
 Query Match
 Black
Pratt
 Staphylococcus aureus protein; ribozyme; antisense sequence; control; Staphylococcal gene; regulatory element; bacterial gene expression; vaccine; Staphylococcal infection; food poisoning; scaled skin syndro
 Staphylococcus
 vaccine; Staphylococcal infection; food toxic shock syndrome.
 AAW28034 standard; Protein;
 Sequence
 Novel polypeptide(s) from Staphylococcus aureus strain WCUH29 - to isolate antimicrobial compounds, and in vaccines against S.
 N-PSDB;
 20-FEB-1996;
 19-FEB-1997;
 WO9730070-A1
 Amino
 27-AUG-1998
 AAW28034;
 (SMIK) SMITHKLINE BEECHAM CORP
 ftp.wipo.int/pub/published_pct_sequences
 1997-424969/39.
 J. M.
 acid
 72
 N
 AAT83988.
 Similarity
 KWEASVPPGSF
 KWEAYITPGAF 12
 Reichard
 Burnham MK,
 sequence
 831 AA;
 Conservative
 (first
 aureus.
 97WO-US02318
 96US-0011888
 RW,
 of the
 entry)
 56.2%;
 82
 Hodgson JE, 1
Rosenberg M,
 English.
 deoxyuridine 5' triphosphatase homologue.
 169
 Score 45;
Pred. No.
 ₽
 Mismatches
 Knowles DJC,
, Ward JM;
 DB
47;
 22;
 2
 Length 831;
 Nicholas
 0;
 used
 Gaps
 0
```

The present sequence represents a Staphylococcus aureus protein, which is believed to be a decxyraidine 5' triphosphatase homologue. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the

Claim

6,

Page 421;

989pp;

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RESULT 10
ABB60901
ID ABB60
 Matches
 Best
 Query Match
 expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect a host against invasion by S. aureus, and conditions relating to Staphylococcal infection, e.g. Staphylococcal food poisoning, scaled skin syndrome, and toxic shock
 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL101840-ABL16175) and the encoded proteins
 Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
Sequence
 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
 New isolated nucleic acid genes from Drosophila and
 N-PSDB; ABL05004.
 WPI; 2001-656860/75
 23-MAR-2000;
11-JUL-2000;
 23-MAR-2001; 2001WO-US09231
 27-SEP-2001
 Drosophila melanogaster
 Drosophila melanogaster polypeptide SEQ ID NO 9495
 26-MAR-2002
 ABB60901;
 ABB60901 standard; Protein; 354
 Sequence
 construction of ribozymes and antisense sequences to control the
 sequences (ABL01840
(ABB57737-ABB72072)
 Disclosure; SEQ ID NO 9495; 21pp + Sequence Listing; English.
 WO200171042-A2
 (PEKE)
 Local
 102
 JC,
 ტ
 Æ
 Similarity 77. 7; Conservative
 YITPGVFDI 110
 YITPGAFDV 14
 CORP NY
 169 AA;
354 AA;
 Adams M,
 (first entry
 2000US-0614150
 2000US-191637P
 55.0%;
77.8%;
 닭
 DWD,
 detection reagent for detecting for elucidating cell signalling
 Score 44; DB Pred. No. 12; 1; Mismatches
 Myers EW;
 ₽
 18; Length 169
 1;
 Indels
 1000
and c
 0;
 cell-cell
 WIPO
 18
 0
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S

Query Match

55.0%;

Score

44; DB 22;

Length 354;

Query Match

55.0%;

Score 44;

멂 24;

Length 369;

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밁
 S
 The invention relates to a complex between two interacting proteins in CC adipocyte cells, given in the specification. The proteins are identified CC by selecting a bait protein from a known adipocyte marker and then CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by CC (RTM) (selected interacting domains) proteins. Also included are a CC polynucleotide encoding a polypeptide in the adipocyte cells, a CC recombinant host cell expressing at least one of the interacting CC polyneptides of the complex, selecting a modulating compound in adipocyte cells, a SID (RTM)) polypeptide comprising any of the 738 maino acid CC cells, a SID (RTM) polynucleotide comprising any of the 738 maino acid CC a SID (RTM) polynucleotide comprising any of the 738 mucleotide sequences given in the specification (including its fragment or variant), a vector CC comprising the vector, a protein chip comprising the polypeptides, a recombinant host cell CC a record comprising all or part of the data, listed in the specification. CC The complex, polypucleotides and compounds are useful for preventing or treating metabolic disorders such as obesity or diabetes. The polypucleotides are useful as probes or primers. The CC complex is particularly useful for identifying selected interacting CC interaction, thus exhibiting the therapeutic effect. The present CC sequence represents a SID (prey) protein of the invention.
 RESULT 11
 Best Local Similarity Matches 7; Conserv
 Human; prey; adipocyte; SID; selected interacting domain; anorectic; antidiabetic; protein-protein interaction; diabetes; yeast 2-hybrid assay; metabolic disorder; obesity.
 New complex between two interacting proteins in adipocyte cells, useful for identifying selected interacting domains that modulate protein interactions, or for preventing or treating metabolic disorders such as
 WPI;
Sequence
 Claim 6; Page 346; 382pp;
 14-MAR-2002; 2002WO-EP03768
 31-OCT-2002.
 Human
 ABU71061 standard; Protein; 369
 N-PSDB;
 Legrain P,
 14-MAR-2001; 2001US-275734P.
 WO200286122-A2
 Homo sapiens
 10-JUN-2003
 ABU71061;
 (HYBR-) HYBRIGENICS
 2003-103412/09
 adipocyte
 31 KWELYMTPNDF 41
 N
 or
 ACA57605
 KWEAYITPGAF
369
 Daviet L;
 Conservative
 (first entry)
 B
 Selected Interacting
 preventing or
 12
 63.6%;
 English.
 1;
 Pred. No.
 A
 Mismatches
 domain,
 27;
 SID,
 ű.
 #692
 Indels
 0;
 Gaps
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RESULT 12
AAG98887
 The method by which to identify agents of a bacterial capacity of the capacity of the proteins. In addition the expression of the proteins, the purified proteins can be used to generate reagents and screen small molecule libraries or other candidate compound libraries for compounds that can be further developed to yield novel antimicrobial compounds. In addition, nucleic acid probes complementary to (I) that are specific for particular species of complementary to (I) that are specific for particular microorganism species of in clinical specimens, therefore, providing a rapid and dependable method by which to identify the causative agents of a bacterial confection. Also, antibodies generated against proteins translated from many transcribed from proliferation-required sequences can also be used to screen for specific microorganisms that produce such proteins in a species-specific manner. AMH84371 and AMH84670 represent sequencing primers used in the isolation of E. coli growth and proliferation related sequence, which are used in an example from the present conference.
 Query Match
Best Local S
Matches 5
 Best Local
Matches
 WPI; 2001-335933/35.
N-PSDB; AAH84558.
 Sequence
 Novel nucleic acids that inhibit Escherichia coli proliferation, useful for screening for homologous genes and for designing expression vectors
 09-NOV-1999;
 09-NOV-2000; 2000WO-US30950
 17-MAY-2001
 AAH84373 to AAH84499 represent Escherichia coli growth and proliferation related DNA sequences (I). AAH84500 to AAH84670 encode the E. coli growth and proliferation related proteins given in AAG99078 and AAG98830 to AAG989999. (I) can be used as potential targets for the generation of
 Claim 19;
 Forsyth RA, Ohlsen K, Zyskind J;
 WO200134810-A2.
 Escherichia coli
 bacterial infection; microorganism.
 Escherichia coli; growth; proliferation; microbial; antimicrobial;
 E. coli growth and proliferation related protein sequence SEQ ID NO:357.
 26-SEP-2001 (first entry)
 AAG98887
 AAG98887 standard; Protein; 867 AA.
 (ELIT-) ELITRA PHARM INC.
 237 WDSYIIPNGFDL 248
 3 WEAYITPGAFDV 14
 3 WEAYITPGAFDV 14
 Similarity 5; Conserv
 Similarity 6; Conserv
 Page 432-434; 522pp; English.
 867
 Conservative
 Conservative
 ÃĂ,
 99US-0164415.
 55.0%;
 50.0%;
 Score 44; DB:
Pred. No. 73;
7; Mismatches
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 Pred. No. 29;
3; Mismatches
 22;
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 Length 867
 Indels
 Indels
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 Gaps
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 RESULT 13
AAG34190
ID AAG34
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 20-MAY-1999;
21-MAY-1999;
24-MAY-1999;
 06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
 14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
 23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
 28-MAY-1999
01-JUN-1999
 25-MAY-1999
27-MAY-1999
 06-SEP-2000
 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
 AAG34190;
 AAG34190 standard;
 14-MAY-1999
 14-MAY-1999
 11-MAY-1999
 04-MAY-1999
 06-APR
 25-FEB-2000;
 EP1033405-A2
 Zea mays subsp. mays.
 termination sequence;
 Zea mays protein fragment SEQ ID NO: 41561
 18-OCT-2000
 14-MAY-1999
 21-APR
 08-APR
 309 YQSYVSPGAFEI 320
 (first entry)
 2000EP-0301439
99US-0138540.
99US-0138847.
99US-0139119.
99US-0139452.
99US-0139453.
99US-0139454.
 99US-0137502.
99US-0137724.
99US-0138094.
 SD66
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-SD66
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S066
S066
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SD66
SD66
 99US
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SD66
SD66
 SU66
 99US
 99US-0130449
 99US-0121825
 Protein;
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RESULT 14
AAG34189
ID AAG34
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 뮍
 5
 Query Match
Best Local S
Matches 6
 17-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
20-AUG-1999
23-AUG-1999
25-AUG-1999
25-AUG-1999
27-AUG-1999
28-SEP-1999
28-SEP-1999
29-SEP-1999
29-SEP-1999
20-SEP-1999
21-OCT-1999
22-OCT-1999
22-OCT-1999
23-OCT-1999
25-OCT-1999
26-OCT-1999
26-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
28-OCT-1999
 AAG34189 standard; Protein;
 83
 1 DKWEAYITPGAFDV ::||| ::| |::
 h 53.8%;
Similarity 42.9%;
6; Conservative
 99US-0149175.
99US-0149722.
99US-0149723.
99US-0149902.
99US-0151065.
99US-0151065.
99US-0151065.
99US-0151065.
99US-0151303.
99US-0151303.
99US-0151303.
99US-0151303.
99US-0151303.
99US-0151303.
99US-0154018.
99US-0154018.
99US-0154018.
99US-0155436.
99US-0155436.
99US-0156596.
99US-0156596.
99US-0156596.
99US-0156596.
99US-0156596.
99US-0156596.
99US-0156596.
99US-01567417.
99US-0156741.
99US-0156767.
99US-0160814.
99US-0160814.
99US-0160814.
99US-0161365.
99US-0161365.
99US-0161365.
99US-0161365.
99US-0161365.
99US-0161365.
99US-0161365.
99US-0161365.
99US-0161361.
 96
 14
 Score 43; DB Pred. No. 23; 5; Mismatches
 217
 B
 21;
 Length
 Indels
 207;
 0,
 Gaps
 0
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99US-01139455.
99US-0139459.
99US-0139451.
99US-0139461.
99US-0139461.
99US-0139462.
99US-0139463.
99US-0139463.
99US-01401543.
99US-0140253.
99US-0141287.
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99US-0141287.
99US-0141287.
99US-0142803.
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99US-0142803.
99US-0142803.
99US-0142803.
99US-0144085.
99US-0144331.
99US-0144332.
99US-0144333.
99US-0145218.
99US-0145218.
99US-0145218.
99US-0145218.
99US-0145218.
99US-0146388.
99US-0147303.
99US-0147433.

22-JUL-1999
22-JUL-1999
22-JUL-1999
22-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
23-JUL-1999
27-JUL-1999
28-JUL-1999
28-JUL-1999
29-AUG-1999
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10-AUG-1999
11-AUG-1999

18-JUN-1999
22-JUN-1999
23-JUN-1999
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11-JUN-1999

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NOTO-	30-APR-1999; 30-APR-1999; 30-APR-1999; 05-MAY-1999; 06-MAY-1999; 06-MAY-1999; 10-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 11-MAY-1999; 12-MAY-1999; 20-MAY-1999; 21-MAY-1999; 21-JUN-1999;	G34189; -OCT-2000 a mays protorial identorial identoria
	99US-0131449. 99US-0132048. 99US-0132484. 99US-0132485. 99US-0132487. 99US-013487. 99US-0134263. 99US-0134218. 99US-013421. 99US-0134708. 99US-0134708. 99US-0134768. 99US-0135221. 99US-0135222. 99US-0136922. 99US-0137528. 99US-0137528. 99US-0137528. 99US-0137524. 99US-0137528. 99US-0137524. 99US-0137528. 99US-0137524. 99US-0137528. 99US-0137524.	rst ent fragme cation,
		ic pathway; 1; promoter;
77	אק אק אין	ה הקי הקי הקי הקי הקי הקי הקי הקי הקי הק
G-1199999999999999999999999999999999999	$^{\circ}$	
9US-01483 9US-01488 9US-01488 9US-01493 9US-01493 9US-01497 9US-01497 9US-01497 9US-01497	903-01445 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01455 903-01457 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477 903-01477	00000000000000000000000000000000000

pathway;
promoter;

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RESULT 15
AAG34188
 Query Match
Best Local
Matches
 25-AUG-1999

27-AUG-1999

27-AUG-1999

27-AUG-1999

27-AUG-1999

30-AUG-1999

31-AUG-1999

31-AUG-1999

31-AUG-1999

31-AUG-1999

10-SEP-1999

10-SEP-1999

12-SEP-1999

22-SEP-1999

23-SEP-1999

23-SEP-1999

24-SEP-1999

24-SEP-1999

23-SEP-1999

24-SEP-1999

24-SEP-1999

24-OCT-1999

25-OCT-1999

14-OCT-1999

14-OCT-1999

14-OCT-1999

12-OCT-1999

14-OCT-1999

21-OCT-1999

22-OCT-1999

22-OCT-1999

22-OCT-1999

23-OCT-1999

25-OCT-1999

25-OCT-1999

26-OCT-1999

26-OCT-1999

26-OCT-1999

27-OCT-1999

27-OCT-1999

28-OCT-1999

29-OCT-1999
 Zea mays protein fragment SEQ
 18-OCT-2000
 AAG34188;
 AAG34188
 Match
 93
 1 DKWEAYITPGAFDV 14

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93 EEWEAILTPEQFNI 106
 Similarity 42.9
6; Conservative
 standard;
 (first entry)
 99US-0150566
99US-0151065
99US-0151065
99US-0151066
99US-0151080
99US-0151303
99US-01513070
99US-0153070
99US-0153070
99US-0154018
99US-0154018
99US-01554018
99US-0155428
99US-0155428
99US-0156458
99US-0159333
99US-0159333
99US-0159333
99US-0160761
99US-0160761
99US-0160761
99US-0160981
99US-0160981
99US-0161404
99US-0161359
99US-0161359
99US-0161359
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Maximum Match 100%
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 Searched:
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 US-09-829-495-63
 Published Applications AA:*
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 GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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US-99-804-320-90
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12 US-10-369-493-18135
US-10-9847-519A-17
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US-09-829-495-63
US-09-972-912-3
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Sequence 3, Appli
Sequence 3, Appli
Sequence 10, Appl
Sequence 5, Appli
Sequence 90, Appl
Sequence 90, Appl
Sequence 18135, A
Sequence 18, Appl
Sequence 82, Appl
Sequence 17, Appl
Sequence 2, Appli
Sequence 2, Appli
Sequence 3985, Ap
Sequence 5, Appli
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### ALIGNMENTS

US-09-832-312-63

Sequence 63, Application US/09832312 Patent No. US20010049829A1

GENERAL INFORMATION:
APPLICANT: Busfield et al.
TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
FILE REFERENCE: 7853-234

CURRENT APPLICATION NUMBER: US/09/832,312
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: 09/610,118
PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: 09/503,387
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: 09/454,824
PRIOR FILING DATE: 1999-12-66
PRIOR APPLICATION NUMBER: 09/345,468

PRIOR FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 78

FastSEQ

for Windows Version 3.0

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; ORCANISM: Homo sapiens
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GENERAL INFORMATION

APPLICANT: Busfield SJ

Jandrot-Perrus M

Vainchenker W

Publication No. US20040001826Al

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CURRENT APPLICATION NUMBER: US/09/829,495

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PRIOR FILING DATE: 2000-06-30

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PRIOR FILING DATE: 2000-02-14

PRIOR APPLICATION NUMBER: 09/454,824

PRIOR FILING DATE: 1999-12-06

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 NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.0620001
TELECOMMUNICATION INFORMATION:
 APPLICATION NUMBER: 09/049,022
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: US/09/972,912
FILING DATE: 10-OCT-2001
CLASSIFICATION: cUnknowns
PRIOR APPLICATION DATA:
 ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 CURRENT APPLICATION DATA:
 CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
 APPLICANT: SOPPET, DANIEL R.

RUBEN, STEVEN M.

TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE
NUMBER OF SEQUENCES: 42
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 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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 TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
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 APPLICANT: Zhou, Jianghong
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
FILE REFERENCE: 07334/109001
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FILE REFERENCE: 07334/109001
CURRENT FILING DATE: 2001-03-12
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/195,896
PRIOR FILING DATE: 1998-11-19
PRIOR FILING DATE: 1998-11-19
PRIOR APPLICATION NUMBER: US 60/108,379
PRIOR FILING DATE: 1998-10-910
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 US-09-972-912-3
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PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US01/41687
PRIOR FILING DATE: 2001-08-10
NUMBER OF SEQ ID NOS: 4
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CURRENT APPLICATION NUMBER: US/10/344,440
CURRENT FILING DATE: 2003-02-10
 APPLICANT: White, David
APPLICANT: Zhou, Jianghong
 APPLICANT: Aroian, Raffi
ORGANISM: Drosophilea melonogaster
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 APPLICANT: White, David
APPLICANT: Zhou, Jianghong
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: LEPTIN INDUCED GENES
FILE REFERENCE: 07334/126001
CURRENT APPLICATION NUMBER: US/09/804,006
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 09/292,228
PRIOR APPLICATION NUMBER: US 60/108,379
PRIOR FILING DATE: 1998-10-29
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PRIOR APPLICATION NUMBER: US 60/108,379
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: US 09/150,857
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US-09-739-451-5
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 US-09-804-006-10
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 ; ORGANISM: Drosophilea melonogaster US-09-804-006-10
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PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/108,928
PRIOR FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 16
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 SOFTWARE: FastSEQ for Windows Version
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Publication No. US20030181408A1
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CURRENT APPLICATION NUMBER: US/09/284,320
CURRENT FILING DATE: 1999-06-21
PRIOR APPLICATION NUMBER: JP 8-301429
PRIOR FILING DATE: 1996-11-13
PRIOR APPLICATION NUMBER: PCT/JP97/04056
PRIOR FILING DATE: 1997-11-07
 CURRENT APPLICATION NUMBER: US/10/287,274
CURRENT FILING DATE: 2002-10-31
PRIOR APPLICATION NUMBER: US 60/164415
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: US 09/711164
PRIOR FILING DATE: 2000-11-09
 APPLICANT: Forsyth, R. Allyn
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETOFILE REFERENCE: ELITEA.008DV1
 TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE DOMAINS AND DNAS TITLE OF INVENTION: ENCODING THESE PROTEINS FILE REFERENCE: GIN-6705CPUS
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 PatentIn Ver. 2.0
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 Application US/09284320
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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LENGTH: 333
TYPE: PRT
ORGANISM: Thermoplasma acidophilum
US-10-369-493-18135
US-09-847-519A-17

Sequence 17, Application US/09847519A

Patent No. US20020102693A1

GENERAL INFORMATION:
APPLICANT: Luche, Ralf M.
APPLICANT: Weil, Bo
TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200115-422

CURRENT APPLICATION UMMBER: US/09/847,519A

CURRENT FILING DATE: 2001-05-01
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 NUMBER OF SEQ ID NOS: 276
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SEQ ID NO 82
LENGTH: 172
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Publication No. US20030170782A1
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Best Local Similarity
 GENERAL INFORMATION:
 Sequence 18135, Application US/10369493
Publication No. US20030233675A1
 APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Coloman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILE REFERENCE: 38-10 ($2052)52
TILE REFERENCE: 38-10 ($2052)52
CURRENT PILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
 CURRENT APPLICATION NUMBER: US/10/091,007
CURRENT FILING DATE: 2002-03-06
PRIOR APPLICATION NUMBER: GB 9921125.2
PRIOR FILING DATE: 1999-09-07
 APPLICANT: Le Page, Richard W F
APPLICANT: Hannify, Sean B
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21978WO
 APPLICANT: Microbial Technics limited APPLICANT: Le Page, Richard W F APPLICANT: Hanniffy, Sean B
 INFORMATION
 199 DSWAGYLSPGEYE 211
 92 YVTPGSFD 99
 1 PKWEAYITPGAFD 13
 6 YITPGAFD 13
 Conservative
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 51.2%;
75.0%;
 38.5%;
 4; Mismatches
 Score 43; DB
Pred. No. 42;
 Score 41; DB
Pred. No. 47;
 Mismatches
 Wells, Jeremy M
 DB 12; Length 172;
 12; Length 333;
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NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PATENTIN VEY. 2.1
; SEQ ID NO 2
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-519A-2
 ; TYPE: PRT; ORGANISM: Homo sapiens US-09-847-519A-17
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; ORGANISM: Neurospora crassa; FEATURE; ; NAME/KEY: unsure; LOCATION: (1)..(868); OTHER INFORMATION: unsure at all Xaa locations US-10-369-493-3985
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 US-09-847-519A-2
 RESULT 13
 US-10-369-493-3985
 RESULT 14
 Sequence 2, Application US/09847519A Patent No. US20020102693A1 GENERAL INFORMATION:
 Query Match 50.0%;
Best Local Similarity 63.6%;
Matches 7; Conservative
 NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
 NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3985
 Sequence 3985, Application US/10369493 Publication No. US20030233675A1
 Best Local Similarity Matches 7; Conserv
 Query Match
 APPLICANT: Luche, Ralf M.
APPLICANT: Wei, Bo
APPLICANT: Wei, Bo
TITLE ONVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125, 422
CURRENT APPLICATION NUMBER: US/09/847,519A
CURRENT FILING DATE: 2001-05-01
 APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
 LENGTH: 86
TYPE: PRT
 LENGTH: 180
 INFORMATION:
 31 EDYCTPGAFEL
 ഗ
 4 EAYITPGAFDV 14
 EAYITPGAFDV 14
 | | |||||::
EDYCTPGAFEL 15
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 50.0%;
 2; Mismatches
 Score 40;
Pred. No.
 Score 40;
Pred. No.
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 DB 10;
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 Length 180
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Sequence 5, Application US/09847539A

Patent No. US2020061306A1

GENERAL INFORMATION:
APPLICANT: Bjorck, Lars H

APPLICANT: Bjorck, Lars H

APPLICANT: Rassmussen, Magnus
ITILE OF INVENTION: STREPTOCOCCAL ALPHA ZM BINDING PROTEIN

FILE REFERENCE: 100084.415US / N.75312B

CURRENT APPLICATION NUMBER: US/09/847,539A

CURRENT FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 141

TYPE: PAT

ORGANISM: Streptococcus pyogenes

US-09-847-539A-5
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Search completed: January 12, 2004, 07:19:54 Job time : 30 secs
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 RESULT 15
US-09-847-539A-5
 Query Match 48.8%; Score 39; DB 9; Length 141; Best Local Similarity 57.1%; Pred. No. 82; Matches 8; Conservative 0; Mismatches 6; Indels
 Query Match 50.0%; Score 40; DB 12; Length 868; Best Local Similarity 63.6%; Pred. No. 3.3e+02; Matches 7; Conservative 2; Mismatches 2; Indels
 2 KWEAYITPGAF 12
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246 RWFAYITLGSF 256
 116 DAWEKAATPIALDV 129
 1 DKWEAYITPGAFDV 14
 0; Gaps
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 0;
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